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# OM protein - protein search, using sw model

Run on: February 22, 2005, 06:37:03 ; Search time 163 Seconds  
(without alignments)  
59.319 Million cell updates/sec

Title: US-10-751-743-4  
Perfect score: 136  
Sequence: 1 CRYTHPHLPRDIYRSTAKAPGRAP 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq\_16Dec04:\*  
1: geneseq19808:\*  
2: geneseq19808:\*  
3: geneseq20008:\*  
4: geneseq20018:\*  
5: geneseq20028:\*  
6: geneseq20038:\*  
7: geneseq20038:\*  
8: geneseq20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 136   | 100.0       | 114    | 6     | ABG74772 Canine Ig  |
| 2          | 136   | 100.0       | 115    | 6     | ABG74774 Human IgE  |
| 3          | 136   | 100.0       | 117    | 6     | ABG74773 Human IgE  |
| 4          | 136   | 100.0       | 124    | 2     | AAW24097 Partial c  |
| 5          | 136   | 100.0       | 312    | 3     | AAV79995 Dog Immun  |
| 6          | 136   | 100.0       | 346    | 6     | ABG74781 Human IgE  |
| 7          | 136   | 100.0       | 347    | 6     | ABG74783 Human CH2  |
| 8          | 136   | 100.0       | 348    | 6     | ABG74782 Human CH2  |
| 9          | 136   | 100.0       | 417    | 2     | AAW23067 Canine Ig  |
| 10         | 136   | 100.0       | 426    | 6     | ABP96583 Dog IgE h  |
| 11         | 136   | 100.0       | 426    | 6     | ABP96583 Dog IgE h  |
| 12         | 120.5 | 88.6        | 341    | 3     | AAAB06208 Immunogen |
| 13         | 115   | 84.6        | 431    | 8     | ADG73237 Cat Immun  |
| 14         | 115   | 84.6        | 431    | 8     | ADG73237 Cat Immun  |
| 15         | 115   | 84.6        | 436    | 6     | ABP96580 Cat IgE h  |
| 16         | 115   | 84.6        | 436    | 6     | ABU09338 Feline Ig  |
| 17         | 115   | 84.6        | 436    | 6     | ABU09338 Feline Ig  |
| 18         | 115   | 84.6        | 436    | 6     | ADG73251 Cat parti  |
| 19         | 105   | 77.2        | 340    | 3     | ABG74776 Rat IgE c  |
| 20         | 105   | 77.2        | 340    | 3     | ABG74776 Rat IgE c  |
| 21         | 105   | 77.2        | 346    | 6     | ABG74785 Human CH2  |
| 22         | 105   | 77.2        | 428    | 6     | ABP96589 Rat IgE h  |
| 23         | 102   | 75.0        | 20     | 2     | AAW24102 Canine im  |
| 24         | 99.5  | 73.2        | 341    | 3     | AAAB06206 Immunogen |
| 25         | 98    | 72.1        | 424    | 5     | AAW50103 Equine Ig  |

|    |      |      |     |   |                     |
|----|------|------|-----|---|---------------------|
| 26 | 98   | 72.1 | 424 | 5 | AAW50104 Equine Ig  |
| 27 | 98   | 72.1 | 569 | 6 | ABP96585 Horse IgE  |
| 28 | 95.5 | 70.2 | 342 | 3 | AAAB06205 Immunogen |
| 29 | 95.5 | 70.2 | 555 | 8 | ADP90027 Oposum-h   |
| 30 | 95.5 | 70.2 | 555 | 8 | ADN00648 ORO pro    |
| 31 | 94   | 69.1 | 567 | 6 | ABP96588 Pig IgE h  |
| 32 | 93.5 | 68.8 | 345 | 3 | AAAB06207 Immunogen |
| 33 | 91.5 | 67.3 | 353 | 8 | ADN00661 H-OCO-H p  |
| 34 | 91.5 | 67.3 | 557 | 8 | ADP90031 Oposum-h   |
| 35 | 91.5 | 67.3 | 557 | 8 | ADP90035 Oposum-h   |
| 36 | 91.5 | 67.3 | 557 | 8 | ADN00656 ORO pro    |
| 37 | 91.5 | 67.3 | 557 | 8 | ADN00652 modOSO     |
| 38 | 91.5 | 67.3 | 566 | 8 | ADP90029 Oposum-h   |
| 39 | 91.5 | 67.3 | 566 | 8 | ADP90037 Oposum-h   |
| 40 | 91.5 | 67.3 | 566 | 8 | ADN00658 ORO-H p    |
| 41 | 91.5 | 67.3 | 566 | 8 | ADN00650 modOSO-H p |
| 42 | 90.5 | 66.5 | 337 | 8 | ADP90022 Oposum-x   |
| 43 | 90.5 | 66.5 | 337 | 8 | ADN00643 ORO prote  |
| 44 | 89   | 65.4 | 17  | 3 | AAV50894 Antibody   |
| 45 | 89   | 65.4 | 17  | 3 | AAV50893 Antibody   |

## ALIGNMENTS

|          |          |   |
|----------|----------|---|
| RESULT 1 | ABG74772 | standard, protein, 114 AA.  |
| ID       | ABG74772 |   |
| XX       | AC       | ABG74772;   |
| XX       | DT       | 05-JUN-2003 (first entry)   |
| XX       | DE       | Canine IgE CH3 domain.  |
| XX       | XX       |   |
| XX       | KM       | CH3 domain; IGF; antigen; non-anaphylactic; anti-IGF; fusion protein;     |
| XX       | KM       | dermatological; anti-inflammatory; ophthalmological; allergy; asthma;     |
| XX       | KM       | allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;  |
| XX       | KM       | conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;    |
| XX       | KM       | gene therapy; dog.  |
| XX       | OS       | Canis familiaris.   |
| XX       | PN       | EP1262491-A2.   |
| XX       | XX       |   |
| XX       | PD       | 04-DEC-2002.  |
| XX       | XX       |   |
| XX       | PF       | 22-MAY-2002; 2002BP-00253606.   |
| XX       | PR       | 22-MAY-2001; 2001US-0292638P.   |
| XX       | PA       | (PF12 ) PFIZER PROD INC.  |
| XX       | PI       | Brown TM, Moresey MA;   |
| XX       | PI       | WPI, 2003-122561/12.  |
| XX       | DR       | N-PSDB; ACAS5170.   |
| XX       | PT       | Novel isolated antigenic peptide comprising amino acid residues of CH3    |
| XX       | PT       | domain of IGF molecule from first species and a second unrelated species, |
| XX       | PT       | induces non-anaphylactic anti-IGF immune response in animal.              |
| XX       | XX       |   |
| XX       | XX       | Claim 15; Page 28; 50pp; English.   |
| XX       | XX       |   |
| XX       | XX       | This invention describes a novel antigenic peptide comprising amino acid  |
| XX       | XX       | residues of an IGF CH3 domain from a first species (ADB1) and amino acid  |
| XX       | XX       | residues of an IGF CH3 domain of a second unrelated species (ADB2), where |
| XX       | XX       | ADB1 is conserved in the IGF CH3 domain of the first species and ADB2 is  |
| XX       | XX       | not conserved in the IGF CH3 domain of the first species. The novel       |
| XX       | XX       | antigenic peptide induces a non-anaphylactic anti-IGF immune response in  |
| XX       | XX       | an animal. The invention also discloses the polynucleotide sequence       |
| XX       | XX       | encoding the antigenic peptide and an antigenic fusion protein comprising |
| XX       | XX       | the antigenic peptide of the invention and a heterologous protein         |

CC carrier, where the fusion protein induces an anti-IGR immune response  
CC that does not cause anaphylaxis when administered to an animal. The  
CC products of the invention have dermatological, antiinflammatory and  
CC ophthalmological activity. The antigenic peptide described is capable of  
CC preventing IGR from binding to high affinity receptors on mast cells and  
CC basophils. The products of the invention are useful in the manufacture  
CC of a medicament for treating or preventing IGR-mediated allergic disorders  
CC including asthma, allergic rhinitis, gastrointestinal allergic disorders  
CC food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea  
CC allergies or atopic dermatitis, in an animal, e.g. human or dog. The  
CC polypeptide products are useful for treating IGE-mediated allergic  
CC disorders. By gene therapy. Antigenic peptides comprising conserved amino  
CC acid residues of the CH3 domain of an IGR molecule from one species  
CC flanked by variable amino acid residues of the CH3 domain of an IGR  
CC molecule from a second unrelated species are capable of inducing a high  
CC titre of anti-IGR antibodies when administered to an animal without  
CC causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences  
CC used in designing the constructs described in the disclosure of the  
CC invention  
XX  
XX Sequence 114 AA;

1 This invention describes a novel antigenic peptide comprising amino acid  
2 residues of an IGE CH3 domain from a first species (ADEx1) and amino acid  
3 residues of an IGE CH3 domain of a second unrelated species (ADEx2), where  
4 ADEx1 is conserved in the IGE CH3 domain of the second species and ADEx2 is  
5 not conserved in the IGE CH3 domain of the first species. The novel  
6 antigenic peptide induces a non-anaphylactic anti-IGE immune response in  
7 an animal. The invention also discloses the polynucleotide sequence  
8 encoding the antigenic peptide and an antigenic fusion protein comprising  
9 the antigenic peptide of the invention and a heterologous protein  
10 carrier, where the fusion protein induces an anti-IGE immune response  
11 that does not cause anaphylaxis when administered to an animal. The  
12 products of the invention have dermatological, antiinflammatory and  
13 ophthalmological activity. The antigenic peptide described is capable of  
14 preventing IGE from binding to high affinity receptors on mast cells and  
15 basophils. The products of the invention are useful in the manufacture of  
16 a medicament for treating or preventing IGE-mediated allergic disorders  
17 including asthma, allergic rhinitis, gastrointestinal allergies such as  
18 food allergies, eczematous dermatitis, conjunctivitis, glomerular nephritis, flea  
19 allergies or atopic dermatitis, in an animal, e.g. human or dog. The  
20 polynucleotide products are useful for treating IGE-mediated allergic  
21 disorders, by gene therapy. Antigenic peptides comprising conserved amino  
22 acid residues of the CH3 domain of an IGE molecule from one species  
23 flanked by variable amino acid residues of the CH3 domain of an IGE  
24 molecule from a second unrelated species are capable of inducing a high  
25 titre of anti-IGE antibodies when administered to an animal without  
26 causing anaphylaxis. AB674772-AB674785 represents polypeptide sequences  
27 used in designing the constructs described in the disclosure of the  
28 invention. (Updated on 23-OCT-2003 to standardise OS field)

|           |   |
|-----------|---|
| XX        | N-PSDBJ; ACAM55171.   |
| DR        |   |
| PT        | Novel isolated antigenic peptide comprising amino acid residues of CH3 domain of IgB molecule from first species and a second unrelated species,  |
| PR        | induces non-anaphylactic anti-IgB immune response in animal.  |
| Pt        |   |
| XX        |   |
| PS        | Claim 2, Page 29, 50pp; English.  |
| XX        |   |
| CC        | This invention describes a novel antigenic peptide comprising amino acid residues of an IgE CH3 domain from a first species (ADE1) and amino acid residues of an IgG CH3 domain of a second unrelated species (ADE2), where ADE1 is conserved in the IgE CH3 domain of the second species and ADE2 is not conserved in the IgE CH3 domain of the first species. The novel antigenic peptide induces a non-anaphylactic anti-IgB immune response in an animal. The invention also discloses the polynucleotide sequence encoding the antigenic peptide and an antigenic fusion protein comprising the antigenic peptide of the invention and a heterologous protein carrier, where the fusion protein induces an anti-IgB immune response that does not cause anaphylaxis when administered to an animal. The products of the invention have dermatological, anti-inflammatory and ophthalmological activity. The antigenic peptide described is capable of preventing IgB from binding to high affinity receptors on mast cells and basophils. The products of the invention are useful in the manufacture of a medicament for treating or preventing IgE-mediated allergic disorders including asthma, allergic rhinitis, gastrointestinal allergies such as food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea allergies or atopic dermatitis, in an animal, e.g. human or dog. The polynucleotide products are useful for treating IgE-mediated allergic disorders, by gene therapy. Antigenic peptides comprising conserved amino acid residues of the CH3 domain of an IgB molecule from one species flanked by variable amino acid residues of the CH3 domain of an IgE molecule form a second unrelated species are capable of inducing a high titre of anti-IgB antibodies when administered to an animal without causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences used in designing the constructs described in the disclosure of the invention |
| CC        |   |
| CC        |   |
| CC        |   |
| CC        |   |
| CC        |   |
| CC        |   |
| CC        |   |
| CC        |   |
| CC        |   |
| CC        |   |
| SQ        | Sequence 117 AA;  |
| XX        |   |
| YY        |   |
| Dy        | Query Match                  100.0%; Score 136; DB 6; Length 117;<br>Best Local Similarity      100.0%; Pred. No. 6,7e-13;<br>Matches        25; Conservative     0; Mismatches     0; Indels     0; Gaps     0;  |
| Db        | 92 CRVTHPHLPKDIVRSIAAKPGKRAP 116<br>     <br>   |
| RESULT 4  |   |
| AAMW24097 | ID    AAW24097 standard; peptide; 124 AA.<br>AAW24097;  |
| AC        | AAW24097;   |
| XX        |   |
| DT        | 21-NOV-1997. (first entry)  |
| XX        |   |
| DE        | Partial canine immunoglobulin B protein.  |
| XX        |   |
| KM        | Immunoglobulin B; IgB; anti-canine IgB antibody; allergy; canine; dog.<br>Canis familiaris.<br>JP09169795-A.  |
| OS        |   |
| XX        |   |
| PD        | 30-JUN-1997.  |
| XX        |   |
| PF        | 22-DEC-1995;    95UP-00334381.  |
| XX        |   |
| PR        | 22-DEC-1995;    95UP-00334381.  |
| XX        |   |
| PA        | (HITB ) HITACHI CHEM CO LTD.  |
| OR        | WPI, 1997-389423/36.  |

|  |   |
|--|---|
| DR   | N-PSDB; AAT6564E.   |
| PT   | Canine immunoglobulin E peptide fragment and related DNA - useful for the preparation of anti-canine immunoglobulin E antibody.   |
| XX   |   |
| XX   |   |
| PS   | Claim 1; Page 8; 12pp; Japanese.  |
| CC   | This is a partial canine immunoglobulin E (IgE) protein. Peptide fragments (AAW24096-106) containing at least five continuous amino acids of this sequence are used for the preparation of anti-canine IgE antibody. The anti-canine IgE antibody can be used for the diagnosis of canine allergies |
| CC   |   |
| CC   |   |
| XX   |   |
| SQ   | Sequence 124 AA;  |
| Dq   |   |
| Db   | 62 CRVTHPHLPDPIVRSTAKAGKCAP 86  |
| Query Match  | 100.0%; Score 136; DB 2; Length 124;<br>Best Local Similarity 100.0%; Pred. No. 7, 2e-13;<br>Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  |
| RESULT 5   |   |
| AAY79995   | standard; protein; 312 AA.  |
| AC   |   |
| AAV79995;  |   |
| DT   | 15-MAY-2000 (first entry)   |
| DE   | Dog Immunoglobulin E epsilon heavy chain SEQ ID NO:2.   |
| KM   | immunoglobulin E; IGH; epsilon heavy chain; antigenic; antigen;   |
| KM   | immunogetic; immunoestimulatory; carrier protein; helper T cell epitope;  |
| KW   | antibody; allergy; allergic disease; immunisation; anti-allergic;   |
| KX   | anti-anaphylactic; anti-aesthetic; asthma; anaphylaxis; dermatitis.   |
| OS   |   |
| Canis sp.  |   |
| PN   | WO967293-A1.  |
| PD   | 29-DEC-1999.  |
| PF   | 21-JUN-1999; 99MO-USO13959.   |
| PR   | 20-JUN-1998; 98US-00100287.   |
| PA   | (UNB-) UNITED BIOMEDICAL INC.   |
| Mang CY,   | Walfield AM;  |
| WI;  | 2000-160578/14.   |
| New antigenic peptide from the CH3 domain of immunoglobulin E, fusions<br>for immunization against allergy.  |   |
| Example 1; Page 66-68; 155pp; English.   |   |
| The present invention describes immunoglobulin E (IGE)-CH3 domain<br>antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and<br>anti-aestmatic properties. (I) induces polyclonal antibodies specific for<br>a target effector site on the epsilon-heavy chain of IgE, and so<br>preventing triggering and activation of mast cells and basophils and<br>downregulation of IgS synthesis. Conjugates, or fusion peptides,<br>containing (I) are used for active immunisation against IgE-mediated<br>allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy<br>dermatitis. Nucleic acids that encode these compounds are useful for<br>recombinant production of corresponding peptides or in DNA vaccines.<br>Conjugates of (I) that include a promiscuous T helper cell epitope<br>(functional in genetically diverse subjects), in addition to a B cell<br>target epitope, have increased immunogenicity and may include cyclic |   |

CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 312 AA;

Query Match 100.0%; Score 136; DB 3; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSIAKAPGKRAP 25  
 DB 192 CRVTHPHLPKDIVRSIAKAPGKRAP 216

RESULT 6  
 ABG74781  
 ID ABG74781 standard; protein; 346 AA.  
 AC ABG74781;  
 XX  
 DT 05-JUN-2003 (first entry)

DE Human IGB CH2-canine CH3-human CH4 IGE-1 fusion protein.

XX CH3 domain; IGE; antigen; non-anaphylactic; anti-IGE; fusion protein;  
 KM dermatological; antiinflammatory; ophthalmological; allergy; asthma;  
 KM allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;  
 KM conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;  
 KM gene therapy; human; canine; dog.

XX Homo sapiens.  
 OS Canis familiaris.

PN EP1262491-A2.

PD 04-DEC-2002.

PF 22-MAY-2002; 2002EP-00253606.

PR 22-MAY-2001; 2001US-0292638P.

PA (PF1Z ) PRIZER PROD INC.

PI Brown TM, Morsey MA;

XX WPI; 2003-122561/12.

DR N-PSDB; ACA55179.

PT Novel isolated antigenic peptide comprising amino acid residues of CH3  
 PT domain of IGE molecule from first species and a second unrelated species,  
 PT induces non-anaphylactic anti-IGE immune response in animal.

PS Claim 3; Page 34-36; 50pp; English.

XX This invention describes a novel antigenic peptide comprising amino acid  
 CC residues of an IGE CH3 domain from a first species (ADB1) and amino acid  
 CC residues of an IGE CH3 domain of a second unrelated species (ADB2), where  
 CC ADB1 is conserved in the IGE CH3 domain of the second species and ADB2 is  
 CC not conserved in the IGE CH3 domain of the first species. The novel  
 CC antigenic peptide induces a non-anaphylactic anti-IGE immune response in  
 CC an animal. The invention also discloses the polynucleotide sequence  
 CC encoding the antigenic peptide and an antigenic fusion protein comprising  
 CC the antigenic peptide of the invention and a heterologous protein  
 CC carrier, where the fusion protein induces an anti-IGE immune response  
 CC that does not cause anaphylaxis when administered to an animal. The  
 CC products of the invention have dermatological, antiinflammatory and  
 CC ophthalmological activity. The antigenic peptide described is capable of  
 CC preventing IGE from binding to high affinity receptors on mast cells and  
 CC basophils. The products of the invention are useful in the manufacture of  
 CC a medicament for treating or preventing IGE-mediated allergic disorders  
 CC including asthma, allergic rhinitis, gastrointestinal allergies such as

CC food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea  
 CC allergies or atopic dermatitis, in an animal, e.g. human or dog. The  
 CC polynucleotide products are useful for treating IGE-mediated allergic  
 CC disorders, by gene therapy. Antigenic peptides comprising conserved amino  
 CC acid residues of the CH3 domain of an IGE molecule from one species  
 CC flanked by variable amino acid residues of the CH3 domain of an IGE  
 CC molecule from a second unrelated species are capable of inducing a high  
 CC titre of anti-IGE antibodies when administered to an animal without  
 CC causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences  
 CC used in designing the constructs described in the disclosure of the  
 CC invention  
 XX  
 SQ Sequence 346 AA;

Query Match 100.0%; Score 136; DB 6; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSIAKAPGKRAP 25  
 DB 217 CRVTHPHLPKDIVRSIAKAPGKRAP 241

RESULT 7  
 ABG74783  
 ID ABG74783 standard; protein; 347 AA.  
 AC ABG74783;  
 XX  
 DT 05-JUN-2003 (first entry)

DE Human CH2-human/canine CH3-human CH4 IGE-3 fusion protein.

XX CH3 domain; IGE; antigen; non-anaphylactic; anti-IGE; fusion protein;  
 KM dermatological; antiinflammatory; ophthalmological; allergy; asthma;  
 KM allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;  
 KM conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;  
 KM gene therapy; human; canine; dog.

XX Homo sapiens.  
 OS Canis familiaris.

PN EP1262491-A2.

PD 04-DEC-2002.

PF 22-MAY-2002; 2002EP-00253606.

PR 22-MAY-2001; 2001US-0292638P.

PA (PF1Z ) PRIZER PROD INC.

PI Brown TM, Morsey MA;

XX WPI; 2003-122561/12.

DR N-PSDB; ACA55181.

PT Novel isolated antigenic peptide comprising amino acid residues of CH3  
 PT domain of IGE molecule from first species and a second unrelated species,  
 PT induces non-anaphylactic anti-IGE immune response in animal.

PS Claim 3; Page 37-39; 50pp; English.

XX This invention describes a novel antigenic peptide comprising amino acid  
 CC residues of an IGE CH3 domain from a first species (ADB1) and amino acid  
 CC residues of an IGE CH3 domain of a second unrelated species (ADB2), where  
 CC ADB1 is conserved in the IGE CH3 domain of the second species and ADB2 is  
 CC not conserved in the IGE CH3 domain of the first species. The novel  
 CC antigenic peptide induces a non-anaphylactic anti-IGE immune response in  
 CC an animal. The invention also discloses the polynucleotide sequence  
 CC encoding the antigenic peptide and an antigenic fusion protein comprising  
 CC the antigenic peptide of the invention and a heterologous protein  
 CC carrier, where the fusion protein induces an anti-IGE immune response

CC that does not cause anaphylaxis when administered to an animal. The  
CC products of the invention have dermatological, anti-inflammatory and  
CC ophthalmological activity. The antigenic peptide described is capable of  
CC preventing Igs from binding to high affinity receptors on mast cells and  
CC basophils. The products of the invention are useful in the manufacture of  
CC a medicament for treating or preventing Igs-mediated allergic disorders  
CC including asthma, allergic rhinitis, gastrointestinal allergies such as  
CC food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea  
CC allergies or atopic dermatitis, in an animal, e.g. human or dog. The  
CC polynucleotide products are useful for treating Igs-mediated allergic  
CC disorders, by gene therapy. Antigenic peptides comprising conserved amino  
CC acid residues of the CH3 domain of an Igs molecule from one species  
CC flanked by variable amino acid residues of the CH3 domain of an Igs  
CC molecule from a second unrelated species are capable of inducing a high  
CC titre of anti-Igs antibodies when administered to an animal without  
CC causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences  
CC used in designing the constructs described in the disclosure of the  
CC invention

SO Sequence 347 AA,  
Query Match 100.0%; Score 136; DB 6; Length 347;  
Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIYRSIAKAPGKRAP 25  
DB 218 CRVTHPHLPDIYRSIAKAPGKRAP 242

RESULT 8  
ABG74782  
ID ABG74782 standard; protein; 348 AA.  
XX  
XX ABG74782;  
XX  
DT 05-JUN-2003 (first entry)  
XX  
XX Human CH2-human/canine CH3-human CH4 Igs-2 fusion protein.  
XX  
XX CH3 domain; Igs; antigen; non-anaphylactic; anti-Igs; fusion protein;  
XX dermatological; anti-inflammatory; ophthalmological; allergy; asthma;  
XX allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia;  
XX conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;  
XX gene therapy; human; canine; dog.  
XX  
XX Homo sapiens.  
XX Canis familiaris.  
XX  
XX EP1262491-A2.  
XX  
XX 04-DEC-2002.  
XX  
XX 22-MAY-2002; 2002BP-00253606.  
XX  
XX 22-MAY-2001; 2001US-0292638P.  
XX  
XX (PF12 ) PFIZER PROD INC.  
XX  
XX Brown TM, Morey MA;  
XX  
XX WPI, 2003-122561/12.  
XX N-PSDB; ACAS5180.  
XX  
XX Novel isolated antigenic peptide comprising amino acid residues of CH3  
XX domain of Igs molecule from first species and a second unrelated species,  
XX induces non-anaphylactic anti-Igs immune response in animal.  
XX  
XX Claim 3, Page 36-37, 50pp; English.  
XX  
XX This invention describes a novel antigenic peptide comprising amino acid  
XX residues of an Igs CH3 domain from a first species (ADG1) and amino acid  
XX residues of an Igs CH3 domain of a second unrelated species (ADE2), where

CC ADE1 is conserved in the Igs CH3 domain of the second species and ADE2 is  
CC not conserved in the Igs CH3 domain of the first species. The novel  
CC antigenic peptide induces a non-anaphylactic anti-Igs immune response in  
CC an animal. The invention also discloses the polynucleotide sequence  
CC encoding the antigenic peptide and an antigenic fusion protein comprising  
CC the antigenic peptide of the invention and a heterologous protein  
CC carrier, where the fusion protein induces an anti-Igs immune response  
CC that does not cause anaphylaxis when administered to an animal. The  
CC products of the invention have dermatological, anti-inflammatory and  
CC ophthalmological activity. The antigenic peptide described is capable of  
CC preventing Igs from binding to high affinity receptors on mast cells and  
CC basophils. The products of the invention are useful in the manufacture of  
CC a medicament for treating or preventing Igs-mediated allergic disorders  
CC including asthma, allergic rhinitis, gastrointestinal allergies such as  
CC food allergies, eosinophilia, conjunctivitis, glomerular nephritis, flea  
CC allergies or atopic dermatitis, in an animal, e.g. human or dog. The  
CC polynucleotide products are useful for treating Igs-mediated allergic  
CC disorders, by gene therapy. Antigenic peptides comprising conserved amino  
CC acid residues of the CH3 domain of an Igs molecule from one species  
CC flanked by variable amino acid residues of the CH3 domain of an Igs  
CC molecule from a second unrelated species are capable of inducing a high  
CC titre of anti-Igs antibodies when administered to an animal without  
CC causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences  
CC used in designing the constructs described in the disclosure of the  
CC invention

SO Sequence 348 AA;  
Query Match 100.0%; Score 136; DB 6; Length 348;  
Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIYRSIAKAPGKRAP 25  
DB 219 CRVTHPHLPDIYRSIAKAPGKRAP 243

RESULT 9  
AAW23067  
ID AAW23067 standard; protein; 417 AA.  
XX  
XX AAW23067;  
XX  
XX 19-FEB-1998 (first entry)  
XX  
XX Canine Igs heavy chain constant region (exon 1-4 product).  
XX  
XX Igs; immunoglobulin; antibody; heavy chain constant region; allergy;  
XX hypersensitivity; therapy; dog; antisense; immunomodulation.  
XX  
XX Canis familiaris.  
XX  
XX Key Location/Qualifiers  
XX  
XX MISC-difference 55  
XX FT /note= "encoded by ACC"  
XX FT MISC-difference 56  
XX FT /note= "encoded by TAC"  
XX FT MISC-difference 67  
XX FT /note= "encoded by GCC"  
XX FT MISC-difference 83  
XX FT /note= "encoded by NNT"  
XX FT MISC-difference 174  
XX FT /note= "encoded by GGN"  
XX FT MISC-difference 175  
XX FT /note= "encoded by NNG"  
XX FT MISC-difference 176  
XX FT /note= "encoded by TGN"  
XX FT MISC-difference 203  
XX FT /note= "encoded by TCC"  
XX FT MISC-difference 204  
XX FT /note= "encoded by GAC"  
XX  
XX WO9730156-A2.

```
XX 21-AUG-1997.
PD 14-FEB-1997; 97WO-US002322.
XX 14-FEB-1996; 96US-00601197.
XX (INDEX-) IDEXX LAB INC.
PA Mermer B, Harris RA, Sieftring AE;
PI WPI; 1997-425031/39.
DR N-PSDB; AAT79278.
XX Isolated canine IGE heavy chain constant region DNA - useful to develop
PT products for treatment of canine allergies and for immunomodulation in
PT dogs.
XX Disclosure; Page 35-39; 59pp; English.
PS This polypeptide is encoded by exons 1-4 (see AAT79278) of canine IGE
CC heavy chain constant region (epsilon) genomic DNA. Another polypeptide,
CC comprising the exon 5 and 6 product, is given in AAW23068. Recombinant
CC peptides encoded by exons 1-6 can be produced in eukaryotic or
CC prokaryotic cells. Such peptides, and antibodies raised against them, are
CC used in methods to treat the manifestation of allergy in dogs, e.g. to
CC treatment Type I immediate hypersensitivity, and for immunomodulation
XX Sequence 417 AA;
SQ
Query Match 100.0%; Score 136; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 2, 8e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRVTHPHLPKDIVRSIAKAPGKRAP 25
DB 289 CRVTHPHLPKDIVRSIAKAPGKRAP 313
RESULT 10
AAR97753 standard; protein; 426 AA.
XX AAR97753;
AC AAR97753;
XX 28-AUG-1996 (first entry)
DT 28-AUG-1996 (first entry)
XX Canine IGE.
DE IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
KM IGE; immunoglobulin; antibody; vaccine; allergy; hypersensitivity.
XX Canis familiaris.
OS Canis familiaris.
XX WO9614867-A1.
PN WO9614867-A1.
XX 23-MAY-1996.
PD 23-MAY-1996.
XX 03-NOV-1995; 95WO-US013795.
PF 03-NOV-1995; 95WO-US013795.
XX 09-NOV-1994; 94US-00336583.
PR 09-NOV-1994; 94US-00336583.
XX (MERI) MERCK & CO INC.
PA (MERI) MERCK & CO INC.
XX Hollis GF, Patel MD;
PI WPI; 1996-277321/28.
DR N-PSDB; AAT29824.
XX New DNA encoding canine IGE and IGA - useful in vaccines, anti-sense
PT therapy, assays, drug screening, etc.
XX Claim 11; Page 29-30; 49pp; English.
```

```
XX The canine IGE amino acid sequence (AAR97753) was deduced from an
CC isolated gene (AAT29824) obtd. from a canine liver DNA library. The
CC cloning of the IGE gene allows prodn. of large quantities of recombinant
CC IGE using bacterial, yeast, mammalian, insect or viral systems. The IGE
CC can be used in drug development (e.g. small molecule screening, assay
CC development and anti-IGE antibody generation). Fragments of IGE can be
CC used in vaccines or to prevent IGE-mediated hypersensitivity. The new
CC sequence information permits targeted modulation of IGE-mediated immune
CC responses
XX Sequence 426 AA;
SQ
Query Match 100.0%; Score 136; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 2, 9e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRVTHPHLPKDIVRSIAKAPGKRAP 25
DB 294 CRVTHPHLPKDIVRSIAKAPGKRAP 318
RESULT 11
ABP96583 standard; protein; 426 AA.
XX ABP96583;
AC ABP96583;
XX 28-MAY-2003 (first entry)
DT 28-MAY-2003 (first entry)
XX Dog IGE heavy chain amino acid sequence SEQ ID NO:28.
DE Dog IGE heavy chain amino acid sequence SEQ ID NO:28.
XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
KM immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;
XX immune response; major histocompatibility complex; MHC; immunogenic;
KM antiallergic; antiaschematic; immunosuppressive; vasotropic; cytostatic;
KM dermatological; antiinflammatory; IGE-mediated condition; food allergy;
KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;
KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
KM urticaria hives.
XX Canis familiaris.
OS Canis familiaris.
XX WO2003015716-A2.
PN WO2003015716-A2.
XX 27-FEB-2003.
PD 27-FEB-2003.
XX 08-AUG-2002; 2002WO-US026986.
PF 08-AUG-2002; 2002WO-US026986.
XX 13-AUG-2001; 2001US-0312120P.
PR 13-AUG-2001; 2001US-0312120P.
XX (IGET-) IGE THERAPEUTICS INC.
PA (IGET-) IGE THERAPEUTICS INC.
XX Chen SA, Yang Y, Barankiewicz T, Chen Z;
PI Chen SA, Yang Y, Barankiewicz T, Chen Z;
XX WPI; 2003-268242/26.
PD WPI; 2003-268242/26.
XX Identifying peptides that induce cytotoxic T-lymphocyte, CTL response
PT against IGE. By identifying peptide eliciting CTL response to IGE
PT peptides naturally presented by major histocompatibility complex class I
PT protein.
XX Example 7; Page 152-154; 187pp; English.
PS The present invention describes a method (M1) for identifying peptides
XX that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin
CC E (IGE), comprising providing a test peptide (T) suspected of being able
CC to bind to major histocompatibility complex (MHC) class I molecule, and
CC evaluating (T) for ability to elicit in a mammal a CTL response to
CC naturally processed and presented IGE peptides, where a peptide that
CC induces such a response is identified. Also described are compositions:
CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);
CC (C2) comprising at least one isolated polynucleotide encoding (I); and
CC (C3) comprising antigen-presenting cells that recognise at least one (I).
```

CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IGE peptides, C1-3 have antiallergic, antisthmatic, immunosuppressive,  
 CC vasoectropic, dermatological, antiinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IGE, and in  
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis, and urticaria  
 CC hives). The present sequence represents an IGE heavy chain amino acid  
 CC sequence, which is given in an example from the present invention  
 XX

SO Sequence 426 AA;

Query Match 100.0%; Score 136; DB 6; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 2, 9e-12;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPDIYRSIAKAPGRAP 25

DB 294 CRVTHPLPDIYRSIAKAPGRAP 318

RESULT 12

AAB06208 AAB06208 standard; protein; 341 AA.

AC AAB06208;

DT 12-SEP-2003 (revised)

DT 22-NOV-2000 (first entry)

XX Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.

XX Dog; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;

XX asthma; eczema; immunogenic peptide.

XX Didelphis virginiana.

XX Canis sp.

XX Chimeric.

PN WO200025722-A2.

PD 11-MAY-2000.

PF 21-OCT-1999; 99WO-SR001896.

PR 02-NOV-1998; 98US-0106652P.

PR 22-SEP-1999; 99US-00401636.

PA (RESI-) RESISTENTIA PHARM AB.

PI Hellman LT;

XX WPI; 2000-365342/31.

PT Immunogenic polypeptides useful for preventing the harmful effects of

PT immunoglobulin E in mammals.

XX Disclosure, Fig 2; 50pp; English.

XX The present sequence is an immunogenic peptide consisting of the heavy  
 CC chain constant regions 2 and 4 of the opossum IGE and the heavy chain  
 CC constant region 3 from the dog. It was shown to cause a stronger  
 CC polyclonal anti-self IGE response than peptides consisting of the same  
 CC regions from one mammal. Immunogenic peptides, particularly those  
 CC consisting of different heavy chain constant regions, can be used for  
 CC vaccination in humans, against bacterial and viral infections and  
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.  
 CC (Updated on 12-SEP-2003 to standardise OS field)

XX SO Sequence 341 AA;

Query Match 88.6%; Score 120.5; DB 3; Length 341;  
 Best Local Similarity 92.3%; Pred. No. 5, 7e-10;  
 Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRVTHPLPDIYRSIAKAPGRAP 25

DB 211 CRVTHPLPDIYRSIAKAPGRAP 236

RESULT 13

ADG73237 ADG73237 standard; protein; 431 AA.

AC ADG73237;

DT 11-MAR-2004 (first entry)

DE Cat immunoglobulin E (IGE) constant region.

XX antiallergic; IGE-modulator; vaccine; feline; IGE; immunoglobulin E;

XX immune response; IGE-mediated response; allergy; cat; constant region.

XX Felis catus.

PN US2003216565-A1.

PD 20-NOV-2003.

PF 07-APR-2003; 2003US-00409772.

PR 07-JAN-1999; 99US-0115033P.

PR 07-JAN-2000; 2000US-00479614.

XX (MCCA/) MCCA.L. C.

PA (WEBE/) WEBER E.

PI Mccall C, Weber E;

XX WPI; 2004-010802/01.

DR N-PSDB; ADG73236.

PS Claim 12; SEQ ID NO 14; 44pp; English.

XX The invention describes an isolated nucleic acid molecule (I) encoding a

XX portion of a feline IGE heavy chain protein. The methods and compositions

XX of the present invention are useful for eliciting feline immune responses

XX for and/or treating IGE-mediated responses, such as allergies. This is

XX the amino acid sequence of a cat immunoglobulin E (IGE) constant region.

XX Sequence 431 AA;

Query Match 84.6%; Score 115; DB 8; Length 431;  
 Best Local Similarity 84.0%; Pred. No. 5, 3e-09;  
 Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRVTHPLPDIYRSIAKAPGRAP 25

DB 299 CRVTHPLPDIYRSIAKAPGRAP 323

RESULT 14

AABP6580 AABP6580 standard; protein; 496 AA.

AC AABP6580;

DT 28-MAY-2003 (first entry)  
 XX Cat IGE heavy chain amino acid sequence SEQ ID NO:25.  
 XX  
 XX Immunoglobulin E; vaccine; IGE; cytotoxic T lymphocyte response;  
 KM immune response; major histocompatibility complex; MHC; immunogenic;  
 KM antiallergic; antiaesthetic; immunosuppressive; vasotropic; cytostatic;  
 KM dermatological; antinflammatory; IGE-mediated condition; food allergy;  
 KM atopic hypersensitivity condition; allergic rhinitis; allergic asthma;  
 KM atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;  
 KM urticaria hives.  
 XX  
 XX Felis catus.  
 OS  
 XX MO2003015716-A2.  
 XX  
 XX 27-FEB-2003.  
 PD  
 XX 08-AUG-2002; 2002MO-US026986.  
 PF  
 XX 13-AUG-2001; 2001US-0312120P.  
 PR  
 XX (IGET-) IGE THERAPEUTICS INC.  
 PA  
 XX Chen SA, Yang Y, Barankiewicz T, Chen Z;  
 PI  
 XX WPI; 2003-268242/26.  
 DR  
 XX  
 PT Identifying peptides that induce cytotoxic T-lymphocyte, CTL response  
 PT against IGE, by identifying peptide eliciting CTL response to IGE  
 PT peptides naturally presented by major histocompatibility complex class I  
 PT protein.  
 PS  
 XX Example 7; Page 145-147; 187pp; English.  
 PS  
 XX The present invention describes a method (M1) for identifying peptides  
 CC that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin  
 CC E (IGE), comprising providing a test peptide (T) suspected of being able  
 CC to bind to major histocompatibility complex (MHC) class I molecule, and  
 CC evaluating (T) for ability to elicit in a mammal a CTL response to  
 CC naturally processed and presented IGE peptides, where a peptide that  
 CC induces such a response is identified. Also described are compositions:  
 CC (C1) comprising at least one immunogenic peptide (I) identified by (M1);  
 CC (C2) comprising at least one isolated polynucleotide encoding (I); and  
 CC (C3) comprising antigen-presenting cells that recognise at least one (I).  
 CC Where C1-3 are able to bind to at least one MHC class I molecule and to  
 CC elicit in a mammal a CTL response to naturally processed and presented  
 CC IGE peptides, C1-3 have antiallergic, antiaesthetic, immunosuppressive,  
 CC vasotropic, dermatological, antinflammatory and cytostatic activities,  
 CC and can be used as inducers of a CTL response against IGE, and in  
 CC vaccines. C1-3 can be used for modulating an IGE-mediated condition in a  
 CC mammal. C1-3 are useful for modulating an IGE-mediated condition such as  
 CC IGE-mediated atopic hypersensitivity condition, IGE-mediated non-atopic  
 CC hypersensitivity condition, IGE myeloma in a mammal. Preferably, C1-3 are  
 CC useful for treating atopic hypersensitivity conditions (such as allergic  
 CC rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-  
 CC atopic hypersensitivity conditions (such as anaphylaxis), and urticaria  
 CC hives). The present sequence represents an IGE heavy chain amino acid  
 CC sequence, which is given in an example from the present invention  
 XX  
 XX  
 SQ Sequence 496 AA;  
 Query Match 84.6%; Score 115; DB 6; Length 496;  
 Best Local Similarity 84.0%; Pred. No. 6.2e-09;  
 Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

ID ABU09338 standard; protein; 496 AA.  
 XX  
 XX AC ABU09338;  
 XX  
 XX DT 27-JUN-2003 (first entry)  
 XX  
 XX DE Feline IGE epsilon heavy chain #2.  
 XX  
 XX KM Feline; immunoglobulin E; IGE epsilon heavy chain; parasitic infection;  
 KM IGE-mediated immune response; allergy; neoplasia; vaccine technology;  
 KM antibody technology; antiallergic; antiparasitic; cytostatic.  
 KM  
 XX  
 XX OS  
 XX Felis catus.  
 XX  
 XX US2003013183-A1.  
 XX  
 XX 16-JAN-2003.  
 XX  
 XX PD  
 XX 07-JAN-2000; 2000US-00479614.  
 PF  
 XX 07-JAN-1999; 99US-0115033P.  
 PR  
 XX (MCCA/) MCCALL C.  
 PA (WEBB/) WEBBER E.  
 PA  
 XX McCall C, Weber E;  
 PI  
 XX WPI; 2003-391997/37.  
 DR  
 XX N-PSDB; ABX95715.  
 DR  
 XX  
 PT New nucleic acid molecule encoding feline immunoglobulin E (IGE) heavy or  
 PT light chain protein, useful for treating feline IGE-mediated responses  
 PT e.g. allergies, parasitic infections or neoplasia.  
 PS  
 XX Claim 1; Page 37-39; 45pp; English.  
 PS  
 XX The present invention relates to the isolation of feline immunoglobulin E  
 CC (IGE) kappa light chain and IGE epsilon heavy chain proteins, and the  
 CC polynucleotide sequences encoding them. The sequences of the invention  
 CC are useful for treating feline IGE-mediated immune responses (e.g.  
 CC allergies, parasitic infections or neoplasia), in vaccine technology,  
 CC small molecule/antibody technology, molecular biology, and various  
 CC immunological techniques related to feline IGE and its functions. The  
 CC present sequence represents feline IGE epsilon heavy chain #2  
 XX  
 XX  
 SQ Sequence 496 AA;  
 Query Match 84.6%; Score 115; DB 6; Length 496;  
 Best Local Similarity 84.0%; Pred. No. 6.2e-09;  
 Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Search completed: February 22, 2005, 06:57:14  
 Job time : 165 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 22, 2005, 06:50:48 ; Search time 42 Seconds

(without alignments)  
44.434 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136  
Sequence: 1 CRVTHPLPDIVRSIAKAPGRAP 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/1/1aa/5B COMB pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A COMB pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B COMB pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS COMB pep: \*  
6: /cgn2\_6/ptodata/1/1aa/backfile1 pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 136   | 100.0       | 312    | 4     | US-09-701-623C-2  |
| 2          | 136   | 100.0       | 426    | 1     | US-08-336-583-2   |
| 3          | 136   | 100.0       | 426    | 5     | PCT-US95-13795-2  |
| 4          | 115   | 84.6        | 71     | 4     | US-09-281-760B-39 |
| 5          | 115   | 84.6        | 107    | 4     | US-09-281-760B-36 |
| 6          | 115   | 84.6        | 431    | 4     | US-09-479-614-14  |
| 7          | 115   | 84.6        | 496    | 4     | US-09-479-614-2   |
| 8          | 115   | 84.6        | 496    | 4     | US-09-479-614-29  |
| 9          | 89    | 65.4        | 17     | 4     | US-09-281-760B-26 |
| 10         | 89    | 65.4        | 25     | 4     | US-09-701-623C-6  |
| 11         | 89    | 65.4        | 45     | 4     | US-09-701-623C-26 |
| 12         | 89    | 65.4        | 45     | 4     | US-09-701-623C-90 |
| 13         | 89    | 65.4        | 46     | 4     | US-09-701-623C-27 |
| 14         | 89    | 65.4        | 57     | 4     | US-09-701-623C-88 |
| 15         | 89    | 65.4        | 62     | 4     | US-09-701-623C-87 |
| 16         | 89    | 65.4        | 63     | 4     | US-09-701-623C-91 |
| 17         | 88    | 64.7        | 313    | 4     | US-09-701-623C-3  |
| 18         | 86    | 63.2        | 325    | 4     | US-09-701-623C-1  |
| 19         | 78    | 57.4        | 106    | 2     | US-08-232-539D-54 |
| 20         | 78    | 57.4        | 109    | 3     | US-08-466-163B-1  |
| 21         | 78    | 57.4        | 109    | 4     | US-09-802-096-1   |
| 22         | 78    | 57.4        | 109    | 4     | US-09-802-077-1   |
| 23         | 78    | 57.4        | 113    | 2     | US-08-232-539D-56 |
| 24         | 72    | 52.9        | 17     | 4     | US-09-281-760B-28 |
| 25         | 72    | 52.9        | 313    | 4     | US-09-701-623C-4  |
| 26         | 69    | 50.7        | 17     | 4     | US-09-281-760B-27 |
| 27         | 69    | 50.7        | 33     | 4     | US-09-701-623C-44 |

|    |      |      |     |   |                    |                    |
|----|------|------|-----|---|--------------------|--------------------|
| 28 | 68   | 50.0 | 25  | 4 | US-09-701-623C-7   | Sequence 7, Appl   |
| 29 | 67.5 | 49.6 | 118 | 3 | US-08-466-151-1    | Sequence 1, Appl   |
| 30 | 67.5 | 49.6 | 119 | 2 | US-08-466-025A-1   | Sequence 1, Appl   |
| 31 | 65   | 47.8 | 17  | 4 | US-09-281-760B-30  | Sequence 30, Appl  |
| 32 | 64   | 47.1 | 25  | 3 | US-09-100-414B-95  | Sequence 95, Appl  |
| 33 | 64   | 47.1 | 25  | 3 | US-09-303-323-95   | Sequence 95, Appl  |
| 34 | 64   | 47.1 | 25  | 4 | US-09-770-014-95   | Sequence 95, Appl  |
| 35 | 64   | 47.1 | 25  | 4 | US-09-701-588C-92  | Sequence 95, Appl  |
| 36 | 64   | 47.1 | 25  | 4 | US-09-701-623C-5   | Sequence 5, Appl   |
| 37 | 64   | 47.1 | 42  | 3 | US-09-100-414B-98  | Sequence 98, Appl  |
| 38 | 64   | 47.1 | 42  | 3 | US-09-100-414B-99  | Sequence 98, Appl  |
| 39 | 64   | 47.1 | 42  | 3 | US-09-100-414B-100 | Sequence 100, Appl |
| 40 | 64   | 47.1 | 42  | 3 | US-09-303-323-98   | Sequence 98, Appl  |
| 41 | 64   | 47.1 | 42  | 3 | US-09-303-323-99   | Sequence 99, Appl  |
| 42 | 64   | 47.1 | 42  | 3 | US-09-303-323-100  | Sequence 100, Appl |
| 43 | 64   | 47.1 | 42  | 4 | US-09-770-014-98   | Sequence 98, Appl  |
| 44 | 64   | 47.1 | 42  | 4 | US-09-770-014-99   | Sequence 99, Appl  |
| 45 | 64   | 47.1 | 42  | 4 | US-09-770-014-100  | Sequence 100, App  |

#### ALIGNMENTS

```
RESULT 1
US-09-701-623C-2
; Sequence 2, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang Ph.D., Chang YI
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 11514153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; PRIOR FILING DATE: 1998-06-20
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Dog
; FEATURES:
; OTHER INFORMATION: CH2CH3n of dog Ige
; PUBLICATION INFORMATION:
; AUTHORS: Patel,
; JOURNAL: Immunogenetics
; VOLUME: 41
; PAGES: 282-286
; DATE: 1995
US-09-701-623C-2
Query Match          100.0%; Score 136; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 2.7e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 CRVTHPLPDIVRSIAKAPGRAP 25
Db      192 CRVTHPLPDIVRSIAKAPGRAP 216
RESULT 2
US-08-336-583-2
; Sequence 2, Application US/08336583
; Patent No. 5629415
; GENERAL INFORMATION:
; APPLICANT: HOLLIS, GREGORY F.
; APPLICANT: PATEL, MAYUR D.
; TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN E
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
```

```
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COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-583-2

Query Match
Best Local Similarity 100.0%; Score 136; DB 1; Length 426;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPGRAP 25
DB 294 CRVTHPLPKDIVRSIAKAPGRAP 318

RESULT 3
PCT-US95-13795-2
Sequence 2, Application PC/RUS9513795
GENERAL INFORMATION:
APPLICANT: HOLLIS, GREGORY P.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13795
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
```

```
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-13795-2

Query Match
Best Local Similarity 100.0%; Score 136; DB 5; Length 426;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPGRAP 25
DB 294 CRVTHPLPKDIVRSIAKAPGRAP 318

RESULT 4
US-09-281-760E-39
Sequence 39, Application US/09281760E
Patent No. 6734287
GENERAL INFORMATION:
APPLICANT: Lawton, Robert
APPLICANT: Mermet, Brian
APPLICANT: Francoeur, Greg
TITLE OF INVENTION: Specific Binding Protein for Treating
FILE REFERENCE: 01-1275A
CURRENT APPLICATION NUMBER: US/09/281,760E
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 09/058,331
PRIOR FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 71
TYPE: PRT
ORGANISM: Canis familiaris
US-09-281-760E-39

Query Match
Best Local Similarity 84.6%; Score 115; DB 4; Length 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSIAKAPG 21
DB 51 CRVTHPLPKDIVRSIAKAPG 71

RESULT 5
US-09-281-760E-36
Sequence 36, Application US/09281760E
Patent No. 6734287
GENERAL INFORMATION:
APPLICANT: Lawton, Robert
APPLICANT: Mermet, Brian
APPLICANT: Francoeur, Greg
TITLE OF INVENTION: Specific Binding Protein for Treating
FILE REFERENCE: 01-1275A
CURRENT APPLICATION NUMBER: US/09/281,760E
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 09/058,331
PRIOR FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 107
TYPE: PRT
ORGANISM: Canis familiaris
FEATURE:
NAME/KEY: misc feature
LOCATION: (136)-(136)
OTHER INFORMATION: "n" stands for any nucleic acid
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FEATURE:
NAME/KEY: misc feature
LOCATION: (413)..(414)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (451)..(451)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (460)..(462)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (500)..(500)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (530)..(530)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (568)..(568)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (847)..(849)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (853)..(853)
OTHER INFORMATION: "n" stands for any nucleic acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (1832)..(1832)
OTHER INFORMATION: "n" stands for any nucleic acid
US-09-281-760E-36

```

```

Query Match      84.6%; Score 115; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CRVTHPLPDIIVRSIAKAPG 21
DB      87 CRVTHPLPDIIVRSIAKAPG 107

```

```

RESULT 6
US-09-479-614-14
; Sequence 14, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-14

```

```

Query Match      84.6%; Score 115; DB 4; Length 431;

```

```

Best Local Similarity 84.0%; Pred. No. 7.7e-10;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 CRVTHPLPDIIVRSIAKAPGKRAP 25
DB      299 CKVTHPDLPDIIVRSIAKAPGRRFP 323

```

```

RESULT 7
US-09-479-614-2
; Sequence 2, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-2

```

```

Query Match      84.6%; Score 115; DB 4; Length 496;
Best Local Similarity 84.0%; Pred. No. 9.1e-10;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 CRVTHPLPDIIVRSIAKAPGKRAP 25
DB      364 CKVTHPDLPDIIVRSIAKAPGRRFP 388

```

```

RESULT 8
US-09-479-614-29
; Sequence 29, Application US/09479614
; Patent No. 6573372
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 29
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Felis catus
US-09-479-614-29

```

```

Query Match      84.6%; Score 115; DB 4; Length 496;
Best Local Similarity 84.0%; Pred. No. 9.1e-10;
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      1 CRVTHPLPDIIVRSIAKAPGKRAP 25
DB      364 CKVTHPDLPDIIVRSIAKAPGRRFP 388

```

```

RESULT 9
US-09-281-760E-26
; Sequence 26, Application US/09281760E
; Patent No. 6734287
; GENERAL INFORMATION:

```

```
/ APPLICANT: Lawton, Robert
/ APPLICANT: Mermier, Brian
/ APPLICANT: Francoeur, Greg
/ TITLE OF INVENTION: Specific Binding Protein for Treating
/ TITLE OF INVENTION: Canine Allergy
/ FILE REFERENCE: 01-1275A
/ CURRENT APPLICATION NUMBER: US/09/281,760E
/ PRIOR FILING DATE: 1999-03-30
/ PRIOR APPLICATION NUMBER: 09/058,331
/ PRIOR FILING DATE: 1998-04-09
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PatSeq for Windows Version 3.0
/ SEQ ID NO 26
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Canis familiaris
US-09-281-760E-26
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```
Query Match      65.4%; Score 89; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 CRVTHPLPKDIVRSI 16
Db      2 CRVTHPLPKDIVRSI 17
```

```
RESULT 10
US-09-701-623C-6
/ Sequence 6, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Yi
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514153US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 25
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-6
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```
Query Match      65.4%; Score 89; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 RVTTHPLPKDIVRSIAK 18
Db      8 RVTTHPLPKDIVRSIAK 24
```

```
RESULT 11
US-09-701-623C-26
/ Sequence 26, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Yi
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514153US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
```

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/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 45
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-26
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Query Match      65.4%; Score 89; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 RVTTHPLPKDIVRSIAK 18
Db      28 RVTTHPLPKDIVRSIAK 44
```

```
RESULT 12
US-09-701-623C-90
/ Sequence 90, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Yi
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514153US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 90
/ LENGTH: 45
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-90
```

```
Query Match      65.4%; Score 89; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 RVTTHPLPKDIVRSIAK 18
Db      28 RVTTHPLPKDIVRSIAK 44
```

```
RESULT 13
US-09-701-623C-27
/ Sequence 27, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Yi
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514153US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
```

```
SEQ ID NO 27
LENGTH: 46
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: I, M, L
NAME/KEY: MOD_RES
LOCATION: (2)
OTHER INFORMATION: S, T
NAME/KEY: MOD_RES
LOCATION: (7)
OTHER INFORMATION: K, L
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: G, R
NAME/KEY: MOD_RES
LOCATION: (9)
OTHER INFORMATION: V, T
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: I, V
NAME/KEY: MOD_RES
LOCATION: (14)
OTHER INFORMATION: I, T
NAME/KEY: MOD_RES
LOCATION: (15)
OTHER INFORMATION: E, R
NAME/KEY: MOD_RES
LOCATION: (16)
OTHER INFORMATION: G, M
NAME/KEY: MOD_RES
LOCATION: (19)
OTHER INFORMATION: F, T
NAME/KEY: MOD_RES
LOCATION: (20)
OTHER INFORMATION: G, M
US-09-701-623C-27
```

```
Query Match          65.4%; Score 89; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 RVTHPHLPKDIVRSIAK 18
Db      29 RVTHPHLPKDIVRSIAK 45
```

```
RESULT 14
US-09-701-623C-88
Sequence 88, Application US/09701623C
Patent No. 6811782
GENERAL INFORMATION:
APPLICANT: Wang Ph.D., Chang Y1
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
FILE REFERENCE: 11514153US1
CURRENT APPLICATION NUMBER: US/09/701,623C
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 88
LENGTH: 57
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
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US-09-701-623C-88

```
Query Match          65.4%; Score 89; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 8.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 RVTHPHLPKDIVRSIAK 18
Db      40 RVTHPHLPKDIVRSIAK 56
```

```
RESULT 15
US-09-701-623C-87
Sequence 87, Application US/09701623C
Patent No. 6811782
GENERAL INFORMATION:
APPLICANT: Wang Ph.D., Chang Y1
TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
FILE REFERENCE: 11514153US1
CURRENT APPLICATION NUMBER: US/09/701,623C
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US99/13959
PRIOR FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: 09/100,287
PRIOR FILING DATE: 1998-06-20
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 87
LENGTH: 62
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-87
```

```
Query Match          65.4%; Score 89; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 9.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2 RVTHPHLPKDIVRSIAK 18
Db      45 RVTHPHLPKDIVRSIAK 61
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Search completed: February 22, 2005, 07:01:02  
Job time : 43 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: February 22, 2005, 07:00:24 ; Search time 131 Seconds

(without alignments)  
62,451 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136  
Sequence: 1 CRVTHPLPDIVRSIAKAPGKRAP 25

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications AA:\*

- 1: /cgn2\_6/prodata/2/pubppa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata/2/pubppa/PCRT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/2/pubppa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/2/pubppa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata/2/pubppa/US07\_NEW\_PUB.pep:\*
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- 7: /cgn2\_6/prodata/2/pubppa/US08\_NEW\_PUB.pep:\*
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- 20: /cgn2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID               | Description        |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1          | 136   | 100.0       | 25     | 9 US-09-938-700-4   | Sequence 4, Appl1  |
| 2          | 136   | 100.0       | 114    | 14 US-10-152-190-1  | Sequence 1, Appl1  |
| 3          | 136   | 100.0       | 115    | 14 US-10-152-190-3  | Sequence 3, Appl1  |
| 4          | 136   | 100.0       | 117    | 14 US-10-152-190-2  | Sequence 2, Appl1  |
| 5          | 136   | 100.0       | 346    | 14 US-10-152-190-10 | Sequence 10, Appl1 |
| 6          | 136   | 100.0       | 347    | 14 US-10-152-190-12 | Sequence 12, Appl1 |
| 7          | 136   | 100.0       | 348    | 14 US-10-152-190-11 | Sequence 11, Appl1 |
| 8          | 136   | 100.0       | 426    | 14 US-10-214-524-28 | Sequence 28, Appl1 |
| 9          | 120.5 | 88.6        | 341    | 9 US-09-401-636-11  | Sequence 11, Appl1 |
| 10         | 120.5 | 88.6        | 341    | 14 US-10-176-664-11 | Sequence 11, Appl1 |
| 11         | 120.5 | 88.6        | 341    | 15 US-10-673-594-11 | Sequence 11, Appl1 |
| 12         | 115   | 84.6        | 431    | 10 US-09-479-614-14 | Sequence 14, Appl1 |
| 13         | 115   | 84.6        | 431    | 15 US-10-409-772-14 | Sequence 14, Appl1 |

|    |      |      |     |                     |                    |
|----|------|------|-----|---------------------|--------------------|
| 14 | 115  | 84.6 | 496 | 10 US-09-479-614-2  | Sequence 2, Appl1  |
| 15 | 115  | 84.6 | 496 | 10 US-09-479-614-29 | Sequence 29, Appl1 |
| 16 | 115  | 84.6 | 496 | 14 US-10-214-524-25 | Sequence 25, Appl1 |
| 17 | 115  | 84.6 | 496 | 15 US-10-409-772-2  | Sequence 2, Appl1  |
| 18 | 115  | 84.6 | 496 | 15 US-10-409-772-29 | Sequence 29, Appl1 |
| 19 | 105  | 77.2 | 114 | 14 US-10-152-190-5  | Sequence 5, Appl1  |
| 20 | 105  | 77.2 | 340 | 9 US-09-401-636-2   | Sequence 2, Appl1  |
| 21 | 105  | 77.2 | 340 | 14 US-10-176-664-2  | Sequence 2, Appl1  |
| 22 | 105  | 77.2 | 340 | 15 US-10-673-594-2  | Sequence 2, Appl1  |
| 23 | 105  | 77.2 | 346 | 14 US-10-152-190-14 | Sequence 14, Appl1 |
| 24 | 105  | 77.2 | 428 | 14 US-10-152-190-34 | Sequence 34, Appl1 |
| 25 | 99.5 | 73.2 | 341 | 9 US-09-401-636-4   | Sequence 4, Appl1  |
| 26 | 99.5 | 73.2 | 341 | 9 US-09-401-636-9   | Sequence 9, Appl1  |
| 27 | 99.5 | 73.2 | 341 | 14 US-10-176-664-4  | Sequence 4, Appl1  |
| 28 | 99.5 | 73.2 | 341 | 14 US-10-176-664-9  | Sequence 9, Appl1  |
| 29 | 99.5 | 73.2 | 341 | 15 US-10-673-594-4  | Sequence 4, Appl1  |
| 30 | 99.5 | 73.2 | 341 | 15 US-10-673-594-9  | Sequence 9, Appl1  |
| 31 | 98   | 72.1 | 424 | 16 US-10-451-078-2  | Sequence 2, Appl1  |
| 32 | 98   | 72.1 | 424 | 16 US-10-451-078-4  | Sequence 4, Appl1  |
| 33 | 98   | 72.1 | 569 | 14 US-10-214-524-30 | Sequence 30, Appl1 |
| 34 | 95.5 | 70.2 | 342 | 9 US-09-401-636-8   | Sequence 8, Appl1  |
| 35 | 95.5 | 70.2 | 342 | 14 US-10-176-664-8  | Sequence 8, Appl1  |
| 36 | 95.5 | 70.2 | 342 | 15 US-10-673-594-8  | Sequence 8, Appl1  |
| 37 | 95.5 | 70.2 | 555 | 15 US-10-438-794-8  | Sequence 8, Appl1  |
| 38 | 95.5 | 70.2 | 555 | 15 US-10-453-915-8  | Sequence 8, Appl1  |
| 39 | 94   | 69.1 | 567 | 14 US-10-214-524-33 | Sequence 33, Appl1 |
| 40 | 93.5 | 68.8 | 345 | 9 US-09-401-636-10  | Sequence 10, Appl1 |
| 41 | 93.5 | 68.8 | 345 | 14 US-10-176-664-10 | Sequence 10, Appl1 |
| 42 | 93.5 | 68.8 | 345 | 15 US-10-673-594-10 | Sequence 10, Appl1 |
| 43 | 91.5 | 67.3 | 353 | 15 US-10-453-915-21 | Sequence 21, Appl1 |
| 44 | 91.5 | 67.3 | 557 | 15 US-10-438-794-12 | Sequence 12, Appl1 |
| 45 | 91.5 | 67.3 | 557 | 15 US-10-438-794-16 | Sequence 16, Appl1 |

## ALIGNMENTS

RESULT 1  
US-09-938-700-4 ; Sequence 4, Application US/0938700  
; Patent No. US20020064525A1  
; GENERAL INFORMATION:  
; APPLICANT: Morsey, et al.  
; TITLE OF INVENTION: Anti-IgB Vaccines  
; FILE REFERENCE: PC10761A  
; CURRENT APPLICATION NUMBER: US/09/938,700  
; CURRENT FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: DOG CH3/CH4 PEPTIDE SEQUENCE  
US-09-938-700-4

Query Match 100.0%; Score 136; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 4,6e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPDIVRSIAKAPGKRAP 25  
DB 1 CRVTHPLPDIVRSIAKAPGKRAP 25

RESULT 2  
US-10-152-190-1  
; Sequence 1, Application US/10152190  
; Publication No. US20030096369A1  
; GENERAL INFORMATION:  
; APPLICANT: Morsey, Mohamad A.  
; TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgB vaccines  
; FILE REFERENCE: PC11011A  
; CURRENT APPLICATION NUMBER: US/10/152,190

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/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 1
/ LENGTH: 114
/ TYPE: PRT
/ ORGANISM: Dog CH3 domain
US-10-152-190-1
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Query Match          100.0%; Score 136; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CRVTHPHLPKDIIVRSIAKAPGKRAP 25
Db 89 CRVTHPHLPKDIIVRSIAKAPGKRAP 113
```

```
RESULT 3
US-10-152-190-3
```

```
/ Sequence 3, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 3
/ LENGTH: 115
/ TYPE: PRT
/ ORGANISM: Human CH3/dog CH3 domain chimera
US-10-152-190-3
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```
Query Match          100.0%; Score 136; DB 14; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CRVTHPHLPKDIIVRSIAKAPGKRAP 25
Db 90 CRVTHPHLPKDIIVRSIAKAPGKRAP 114
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```
RESULT 4
US-10-152-190-2
```

```
/ Sequence 2, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 2
/ LENGTH: 117
/ TYPE: PRT
/ ORGANISM: Human CH3/dog CH3 domain fusion
US-10-152-190-2
```

```
Query Match          100.0%; Score 136; DB 14; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CRVTHPHLPKDIIVRSIAKAPGKRAP 25
Db 92 CRVTHPHLPKDIIVRSIAKAPGKRAP 116
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RESULT 5

```
US-10-152-190-10
/ Sequence 10, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 10
/ LENGTH: 346
/ TYPE: PRT
/ ORGANISM: IGF-1 fusion protein
US-10-152-190-10
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```
Query Match          100.0%; Score 136; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 8.4e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 CRVTHPHLPKDIIVRSIAKAPGKRAP 25
Db 217 CRVTHPHLPKDIIVRSIAKAPGKRAP 241
```

```
RESULT 6
US-10-152-190-12
```

```
/ Sequence 12, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 12
/ LENGTH: 347
/ TYPE: PRT
/ ORGANISM: IGF-3 fusion protein
US-10-152-190-12
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```
Query Match          100.0%; Score 136; DB 14; Length 347;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CRVTHPHLPKDIIVRSIAKAPGKRAP 25
Db 218 CRVTHPHLPKDIIVRSIAKAPGKRAP 242
```

```
RESULT 7
US-10-152-190-11
```

```
/ Sequence 11, Application US/10152190
/ Publication No. US20030096369A1
/ GENERAL INFORMATION:
/ APPLICANT: Morsey, Mohamed A.
/ TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IGF vaccines
/ FILE REFERENCE: PC11011A
/ CURRENT APPLICATION NUMBER: US/10/152,190
/ CURRENT FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 11
/ LENGTH: 348
/ TYPE: PRT
/ ORGANISM: IGF-2 fusion protein
US-10-152-190-11
```

```
Query Match          100.0%; Score 136; DB 14; Length 348;
Best Local Similarity 100.0%; Pred. No. 8.5e-11;
```



```
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRVTHPHLPDIYRSIAKAPGKRAP 25
Db 219 CRVTHPHLPDIYRSIAKAPGKRAP 243

RESULT 8
US-10-214-524-28
; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Swei-Shen Alex
; APPLICANT: Barankiewicz, Theresa J.
; APPLICANT: Yang, Yong-Min
; APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGB-00101.P.1.1
; CURRENT APPLICATION NUMBER: US/10/214,524
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28

Query Match 100.0%; Score 136; DB 14; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRVTHPHLPDIYRSIAKAPGKRAP 25
Db 294 CRVTHPHLPDIYRSIAKAPGKRAP 318

RESULT 9
US-09-401-636-11
; Sequence 11, Application US/09401636
; Patent No. US20010038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-11

Query Match 88.6%; Score 120.5; DB 9; Length 341;
Best Local Similarity 92.3%; Pred. No. 1.3e-08;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CRVTHPHLPDIYRSIAKAPGKRAP 25
Db 211 CRVTHPHLPDIYRSIAKAPGKRAP 236

RESULT 10
US-10-176-664-11
; Sequence 11, Application US/10176664
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```
; Publication No. US20030031663A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/176,664
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-11

Query Match 88.6%; Score 120.5; DB 14; Length 341;
Best Local Similarity 92.3%; Pred. No. 1.3e-08;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CRVTHPHLPDIYRSIAKAPGKRAP 25
Db 211 CRVTHPHLPDIYRSIAKAPGKRAP 236

RESULT 11
US-10-673-594-11
; Sequence 11, Application US/10673594
; Publication No. US2004007625A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/006001
; CURRENT APPLICATION NUMBER: US/10/673,594
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US/09/401,636
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/106,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-11

Query Match 88.6%; Score 120.5; DB 15; Length 341;
Best Local Similarity 92.3%; Pred. No. 1.3e-08;
Matches 24; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 CRVTHPHLPDIYRSIAKAPGKRAP 25
Db 211 CRVTHPHLPDIYRSIAKAPGKRAP 236

RESULT 12
US-09-479-614-14
; Sequence 14, Application US/09479614
; Publication No. US2003003183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
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;; CURRENT FILING DATE: 2000-01-07  
;; EARLIER APPLICATION NUMBER: 60/115,033  
;; EARLIER FILING DATE: 1999-01-07  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 14  
;; LENGTH: 431  
;; TYPE: PRT  
;; ORGANISM: Felis catus  
US-09-479-614-14

Query Match 84.6%; Score 115; DB 10; Length 431;  
Best Local Similarity 84.0%; Pred. No. 9,7e-08;  
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25  
Db 299 CQVTHPDLPKDIVRSIAKAPGRRFP 323

## RESULT 13

US-10-409-772-14  
;; Sequence 14, Application US/10409772  
;; Publication No. US20030216565A1  
;; GENERAL INFORMATION:  
;; APPLICANT: McCall, Catherine  
;; APPLICANT: Weber, Eric  
;; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
;; FILE REFERENCE: P-1047  
;; CURRENT APPLICATION NUMBER: US/10/409,772  
;; CURRENT FILING DATE: 2003-04-07  
;; PRIOR APPLICATION NUMBER: US/09/479,614  
;; PRIOR FILING DATE: 2000-01-07  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 14  
;; LENGTH: 431  
;; TYPE: PRT  
;; ORGANISM: Felis catus  
US-10-409-772-14

Query Match 84.6%; Score 115; DB 15; Length 431;  
Best Local Similarity 84.0%; Pred. No. 9,7e-08;  
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25  
Db 299 CQVTHPDLPKDIVRSIAKAPGRRFP 323

RESULT 14  
US-09-479-614-2  
;; Sequence 2, Application US/09479614  
;; Publication No. US20030013183A1  
;; GENERAL INFORMATION:  
;; APPLICANT: McCall, Catherine  
;; APPLICANT: Weber, Eric  
;; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
;; FILE REFERENCE: P-1047  
;; CURRENT APPLICATION NUMBER: US/09/479,614  
;; CURRENT FILING DATE: 2000-01-07  
;; EARLIER APPLICATION NUMBER: 60/115,033  
;; EARLIER FILING DATE: 1999-01-07  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 2  
;; LENGTH: 496  
;; TYPE: PRT  
;; ORGANISM: Felis catus  
US-09-479-614-2

Query Match 84.6%; Score 115; DB 10; Length 496;  
Best Local Similarity 84.0%; Pred. No. 1,1e-07;

Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25  
Db 364 CQVTHPDLPKDIVRSIAKAPGRRFP 388

RESULT 15  
US-09-479-614-29  
;; Sequence 29, Application US/09479614  
;; Publication No. US20030013183A1  
;; GENERAL INFORMATION:  
;; APPLICANT: McCall, Catherine  
;; APPLICANT: Weber, Eric  
;; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods  
;; FILE REFERENCE: P-1047  
;; CURRENT APPLICATION NUMBER: US/09/479,614  
;; CURRENT FILING DATE: 2000-01-07  
;; EARLIER APPLICATION NUMBER: 60/115,033  
;; EARLIER FILING DATE: 1999-01-07  
;; NUMBER OF SEQ ID NOS: 34  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 29  
;; LENGTH: 496  
;; TYPE: PRT  
;; ORGANISM: Felis catus  
US-09-479-614-29

Query Match 84.6%; Score 115; DB 10; Length 496;  
Best Local Similarity 84.0%; Pred. No. 1,1e-07;  
Matches 21; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSIAKAPGRAP 25  
Db 364 CQVTHPDLPKDIVRSIAKAPGRRFP 388

Search completed: February 22, 2005, 07:14:10  
Job time : 132 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2005, 06:51:23 / Search time 38 Seconds

(without alignments)  
63.301 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136

Sequence: 1 CRVTHPHLPKDIYRSIAKAPGRAP 25

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 105   | 77.2        | 429    | 1 EHRT   | Ig epsilon chain C |
| 2          | 89    | 65.4        | 426    | 2 I36948 | Ig epsilon chain C |
| 3          | 86    | 63.2        | 428    | 1 EKHU   | Ig epsilon chain C |
| 4          | 80    | 58.8        | 388    | 1 EHM5   | Ig epsilon chain C |
| 5          | 80    | 58.8        | 548    | 2 S3864  | Ig epsilon chain C |
| 6          | 67    | 49.3        | 107    | 2 I68726 | Ig epsilon chain C |
| 7          | 67    | 49.3        | 107    | 2 I68730 | Ig epsilon chain C |
| 8          | 59    | 43.4        | 684    | 2 S60266 | Ig epsilon chain C |
| 9          | 58    | 42.6        | 549    | 2 S04845 | Ig epsilon chain C |
| 10         | 54    | 39.7        | 1938   | 1 S06005 | Ig epsilon chain C |
| 11         | 54    | 39.7        | 1939   | 1 A46762 | Ig epsilon chain C |
| 12         | 54    | 39.7        | 1939   | 2 I48175 | Ig epsilon chain C |
| 13         | 52    | 38.2        | 273    | 2 B87319 | Ig epsilon chain C |
| 14         | 51    | 37.5        | 572    | 2 B45629 | Ig epsilon chain C |
| 15         | 51    | 37.5        | 572    | 2 B45629 | Ig epsilon chain C |
| 16         | 51    | 37.5        | 1938   | 2 I49464 | Ig epsilon chain C |
| 17         | 51    | 37.5        | 1940   | 1 A24932 | Ig epsilon chain C |
| 18         | 51    | 37.5        | 1940   | 1 S04090 | Ig epsilon chain C |
| 19         | 50.5  | 37.1        | 277    | 2 I47162 | Ig epsilon chain C |
| 20         | 50.5  | 37.1        | 327    | 1 G4HU   | Ig epsilon chain C |
| 21         | 50.5  | 37.1        | 328    | 2 I47160 | Ig epsilon chain C |
| 22         | 50.5  | 37.1        | 328    | 2 I47161 | Ig epsilon chain C |
| 23         | 50.5  | 37.1        | 328    | 2 I47158 | Ig epsilon chain C |
| 24         | 50.5  | 37.1        | 328    | 2 I47159 | Ig epsilon chain C |
| 25         | 50.5  | 37.1        | 330    | 1 G2MSA  | Ig epsilon chain C |
| 26         | 50.5  | 37.1        | 330    | 1 G2MSAM | Ig epsilon chain C |
| 27         | 50.5  | 37.1        | 446    | 2 S40295 | Ig epsilon chain C |
| 28         | 50.5  | 37.1        | 469    | 2 S37483 | Ig epsilon chain C |
| 29         | 50.5  | 37.1        | 538    | 2 A83972 | Ig epsilon chain C |

|    |      |      |      |          |                    |
|----|------|------|------|----------|--------------------|
| 30 | 50   | 36.8 | 1038 | 1 MWRBCB | myosin beta heavy  |
| 31 | 50   | 36.8 | 1934 | 2 I48153 | myosin beta heavy  |
| 32 | 50   | 36.8 | 1935 | 1 A37102 | myosin beta heavy  |
| 33 | 50   | 36.8 | 1935 | 1 S06006 | myosin beta heavy  |
| 34 | 50   | 36.8 | 1935 | 2 A59286 | myosin beta heavy  |
| 35 | 49.5 | 36.4 | 405  | 1 G2MSBM | Ig epsilon chain C |
| 36 | 49.5 | 36.4 | 474  | 1 G2MS11 | Ig epsilon chain C |
| 37 | 49.5 | 36.4 | 573  | 2 G12838 | Ig epsilon chain C |
| 38 | 49.5 | 36.0 | 1937 | 2 I38055 | Ig epsilon chain C |
| 39 | 49.5 | 36.0 | 1938 | 1 JX0178 | Ig epsilon chain C |
| 40 | 48.5 | 35.7 | 166  | 2 C72641 | Ig epsilon chain C |
| 41 | 48.5 | 35.7 | 234  | 2 PT0207 | Ig epsilon chain C |
| 42 | 48.5 | 35.7 | 255  | 4 S31866 | Ig epsilon chain C |
| 43 | 48.5 | 35.7 | 329  | 2 S00847 | Ig epsilon chain C |
| 44 | 48.5 | 35.7 | 330  | 1 G4HU   | Ig epsilon chain C |
| 45 | 48.5 | 35.7 | 374  | 2 S69339 | Ig epsilon chain C |

## ALIGNMENTS

## RESULT 1

EHRT  
Ig epsilon chain C region - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text\_change 09-Jul-2004  
C/Accession: A93442; A90937; A02143  
R/Hellman, L.; Pelterson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.  
Nucleic Acids Res. 10, 6041-6049, 1982  
A/Title: Structure and evolution of the heavy chain from rat immunoglobulin E.  
A/Reference number: A93442; PMID:83064537; PMID:6292865  
A/Accession: A93442  
A/Molecule type: mRNA  
A/Residues: 1-429 <HL>  
A/Cross-references: UNIPROT:P01855  
A/Experimental source: strain I/O/c/Wsl, immunocytoma IR2  
R/Kinderogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.  
DNA 1, 335-343, 1982  
A/Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, A/Reference number: A90937; PMID:83182019; PMID:6820340  
A/Contents: myeloma IR162  
A/Accession: A90937  
A/Molecule type: mRNA  
A/Residues: N', 169-307, 'U', 309-342 <KIN>  
C/Complex: An immunoglobulin heterodimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1, C/Superfamily: immunoglobulin C region; immunoglobulin homology  
C/Keywords: duplication; glycoprotein; heterodimer; immunoglobulin  
P/19-80/Domain: immunoglobulin homology <IM1>  
P/118-186/Domain: immunoglobulin homology <IM2>  
P/223-291/Domain: immunoglobulin homology <IM3>  
P/327-398/Domain: immunoglobulin homology <IM4>  
P/46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predict.

Query Match 77.2%, Score 105, DB 1; Length 429;  
Best Local Similarity 79.2%, Pred. No. 2.6e-07;  
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIYRSIAKAPGRAP 24  
DB 289 CRVTHPHLPKDIYRSIAKAPGRAP 312

RESULT 2  
I36948  
Ig epsilon chain - chimpanzee (fragment)  
C/Species: Pan troglodytes (chimpanzee)  
C/Date: 04-Oct-1996 #sequence revision 04-Oct-1996 #text\_change 21-Jan-2000  
C/Accession: I36948  
R/Sakoyama, Y.; Hong, K.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987  
A/Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangutan  
A/Reference number: I36948; MUID:87147196; PMID:3103123

US-10-751-743-4.open.rpx

```

//Accession: J36948
A:/status: preliminary; translated from GB/EMBL/DDBJ
A:/molecule type: DNA
A:/cleidues: type: DNA
A:/cross-references: GB:M15398; NID:g176797; PIDN:AAA5416.1; PID:g176798
A:/genetics: references: GB:M15398; NID:g176797; PIDN:AAA5416.1; PID:g176798
C:/strutrons: 103/1; 209/1; 317/1
F:/336-405/Domains: Immunoglobulin C region, immunoglobulin homology <IMM>
Query Match
Best Local Similarity 65.4%; Score 89; DB 2; Length 426;
Matches 16; Conservative 2; Mismatches 6; Indels 0; Gaps 0
    1 CRVTHPLPKDIVRSIMAKAGKA 24
      |||||:::|||||
297 CRVTHPLKALVALVSTTKTSGPRA 320
      |||||:::|||||
RESULT 3
HHHU

```

[illegible]

| Best Match            | Interchain (Hydrophobic) | Chains            | #Residues              |
|-----------------------|--------------------------|-------------------|------------------------|
| Best Local Similarity | 63.2%                    | Score 86          | #Residues Predicted    |
| Matches 15            | Conservative 62.5%       | Pred. No. 0.00014 | #Residues Experimental |
|                       |                          | 3, Mismatches 6   | Indels 0, Gaps 0       |

OY 1 CRVTHPHLPKDIYRSIAKAPGKRA 24  
 |||||: :|||  
 DB 299 CRVTHPHLPKALNRSTTKTGSPRA 322

## RESULT 4

EMMS  
 Ig epsilon chain C region (version 1) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 13-Jun-1993 #sequence\_revision 13-Jun-1993 #text\_change 09-Jul-2004  
 C/Accession: A02144  
 R/Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982  
 A/Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.  
 A/Reference number: A02144; MUID:83117774; PMID:6818553  
 A/Accession: A02144  
 A/Molecule type: mRNA  
 A/Residues: 1-388 <LIU>

C/Cross-references: UNIPROT:P06336; GB:J00476; NID:G194875; PIDN:AAA38085.1; PID:G387220  
 C/Complex: An immunoglobulin heterotrimeric subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin  
 F/1-44/Domain: immunoglobulin homology (fragment) <IM1>  
 F/81-149/Domain: immunoglobulin homology <IM2>  
 F/186-254/Domain: immunoglobulin homology <IM3>  
 F/280-361/Domain: immunoglobulin homology <IM4>  
 F/10,51,62,133,205,228,332,382/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 58.8%; Score 80; DB 1; Length 388;  
 Best Local Similarity 62.5%; Pred. No. 0.00094;  
 Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRVTHPHLPKDIYRSIAKAPGKRA 24  
 |||||: :|||  
 DB 252 CIVDHPDPKPKYRSITKTPGQRS 275

## RESULT 5

Ig epsilon chain C region - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-May-2001  
 C/Accession: S38864  
 R/Kipp, B.; Becker, W.; Schlaak, M.  
 Submitted to the EMBL Data Library, November 1993  
 A/Description: Combination of a defined specificity and desired isotype by cloning of an A/Reference number: S38864  
 A/Accession: S38864  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-548 <KIP>  
 A/Cross-references: EMBL:Z27397; NID:G416537; PIDN:CAA81788.1; PID:G940782  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 F/333-421/Domain: immunoglobulin homology <IM5>

Query Match 58.8%; Score 80; DB 2; Length 548;  
 Best Local Similarity 62.5%; Pred. No. 0.0013;  
 Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRVTHPHLPKDIYRSIAKAPGKRA 24  
 |||||: :|||  
 DB 419 CIVDHPDPKPKYRSITKTPGQRS 442

## RESULT 6

IGB chain C3 region - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jan-2000  
 C/Accession: I68726  
 R/Shinkai, Y.; Nakachi, H.; Honjo, T.; Okumura, K.  
 Immunogenetics 27, 288-292, 1988

A/Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid  
 A/Reference number: I54443; MUID:88152907; PMID:3346043

A/Accession: I68726  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-107 <RES>  
 A/Cross-references: GB:M22930; NID:G194455; PIDN:AAA37911.1; PID:G194460  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 F/22-90/Domain: immunoglobulin homology <IM6>

Query Match 49.3%; Score 67; DB 2; Length 107;  
 Best Local Similarity 65.0%; Pred. No. 0.019;  
 Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRVTHPHLPKDIYRSIAKAP 20  
 |||||: :|||  
 DB 88 CIVDHPDPKPKYRSITKTP 107

## RESULT 7

IGB chain C3 region - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jan-2000  
 C/Accession: I68730  
 R/Shinkai, Y.; Nakachi, H.; Honjo, T.; Okumura, K.  
 Immunogenetics 27, 288-292, 1988

A/Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid  
 A/Reference number: I54443; MUID:88152907; PMID:3346043

A/Accession: I68730  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-107 <RES>  
 A/Cross-references: GB:M22933; NID:G194464; PIDN:AAA37915.1; PID:G194469  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 F/22-90/Domain: immunoglobulin homology <IM6>

Query Match 49.3%; Score 67; DB 2; Length 107;  
 Best Local Similarity 65.0%; Pred. No. 0.019;  
 Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRVTHPHLPKDIYRSIAKAP 20  
 |||||: :|||  
 DB 88 CIVDHPDPKPKYRSITKTP 107

## RESULT 8

novel antigen receptor precursor - nurse shark  
 C/Species: Ginglymostoma cirratum (nurse shark)  
 C/Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004  
 C/Accession: S60266  
 J/Greenberg, A.S.; Avila, D.; Hughes, M.; McKinney, E.C.; Flajnik, M.F.  
 Nature 374, 168-173, 1995  
 A/Title: A new antigen receptor gene family that undergoes rearrangement and extensive  
 A/Reference number: S60266; MUID:95183140; PMID:787689  
 A/Accession: S60266  
 A/Status: preliminary; nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-684 <GRS>  
 A/Cross-references: UNIPROT:Q90544; EMBL:U18701; NID:G699442; PIDN:ABA8195.1; PID:G6999.

Query Match 43.4%; Score 59; DB 2; Length 684;  
 Best Local Similarity 50.0%; Pred. No. 1.7;  
 Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRVTHPHLPKDIYRSIAKAP 22  
 |||||: :|||  
 DB 645 CIVGHPSLNRDLIRSTRKSNKG 666

## RESULT 9

IGB chain C3 region - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 21-Jan-2000  
 C/Accession: I68726  
 R/Shinkai, Y.; Nakachi, H.; Honjo, T.; Okumura, K.  
 Immunogenetics 27, 288-292, 1988

Ig heavy chain precursor - African clawed frog (fragment)  
 C/Species: Xenopus laevis (African clawed frog)  
 C/Date: 12-Feb-1993 #sequence (revision 12-Feb-1993 #text\_change 26-Aug-1999  
 A/Accession: S04845; S05695  
 R/Mahdavi, C.T.; Haire, R.N.; Litman, G.W.  
 Nucleic Acids Res. 17, 5388, 1989  
 A/Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin  
 A/Reference number: S04845; MUID:89345103; PMID:2503814  
 A/Accession: S04845  
 A/Molecule type: mRNA  
 A/Residues: 1-549 <AMB>  
 A/Cross-references: EMBL:X15114  
 R/Litman, G.W.  
 submitted to the EMBL Data Library, April 1989  
 A/Reference number: S05695  
 A/Accession: S05695  
 A/Molecule type: mRNA  
 A/Residues: 'LC', 3-308, 'H', 310-549 <LT>  
 A/Cross-references: EMBL:X15114; NID:964799; PID:G763031  
 C/Superfamily: immunoglobulin C region; immunoglobulin homology  
 C/Keywords: glycoprotein; heterotrimer; immunoglobulin homology  
 F, 26-109/Domain: immunoglobulin homology <IMM>  
 F, 281, 294/Binding site: carbohydrate (Aam) (covalent) #status predicted

Query Match      42.6%;      Score 58;      DB 2;      Length 549;  
 Best Local Similarity      52.2%;      Pred. No. 1.9;  
 Matches      12;      Conservative      3;      Mismatches      6;      Indels      2;      Gaps      1;

QY      1      CRYTHRLPKDLYRSIAKA--PG 21  
 DB      424      CKVHPDLPSPIKSIQKSDPG 446

RESULT 10  
 S06005  
 myosin alpha heavy chain, cardiac muscle [similarity] - rat  
 N/Alternate names: alpha-myosin heavy chain  
 N/Contains: myosin ATPase (EC 3.6.4.1)  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 31-Dec-1993 #sequence (revision 31-Dec-1993 #text\_change 09-Jul-2004  
 A/Accession: S06005; S07535; A20971; A02988; I53305  
 R/McNally, E.M.; Glanola, K.M.; Leinwand, L.A.  
 Nucleic Acids Res. 17, 7527-7528, 1989  
 A/Title: Complete nucleotide sequence of full length cDNA for rat alpha cardiac myosin h  
 A/Reference number: S06005; MUID:90016822; PMID:2798111  
 A/Accession: S06005  
 A/Status: translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-1938 <MCN>  
 A/Cross-references: UNIPROT:P02563; EMBL:X15938; NID:956654; PIDN:CAA34064.1; PID:956655  
 R/McNally, E.M.; Kraft, R.; Bryvo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.  
 J. Mol. Biol. 210, 665-671, 1989  
 A/Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Comparison  
 A/Reference number: S07535; MUID:9013919; PMID:2614840  
 A/Accession: S07535  
 A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-1938 <MC2>  
 R/Mahdavi, V.; Chambers, A.P.; Nadal-Ginard, B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 2626-2630, 1984  
 A/Title: Cardiac alpha- and beta-myosin heavy chain genes are organized in tandem.  
 A/Reference number: A20971; MUID:84194059; PMID:6585819  
 A/Accession: A20971  
 A/Molecule type: protein  
 A/Residues: 1-12, 'AP', 14-45, 'A', 47-50, 'AP', 53-81, 'E', 83-86, 'Q', 88-109, 111-133, 'H', 135-16  
 R/Mahdavi, V.; Perlasamy, M.; Nadal-Ginard, B.  
 Nature 297, 659-664, 1982  
 A/Title: Molecular characterization of two myosin heavy chain genes expressed in the adu  
 A/Reference number: A02988; MUID:82220036; PMID:7045682  
 A/Accession: A02988  
 A/Molecule type: mRNA  
 A/Residues: 1512-1574, 'S', 1576-1721, 'N', 1723-1851, 'N', 1853-1869, 'N', 1871-1933, 'I', 1935-1  
 A/Note: There are 10 or more myosin heavy chain genes in the rat, at least two of which

R/Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.  
 Eur. Heart J. 5, 181-191, 1984  
 A/Title: Cardiac myosin heavy chain isozytic transitions during development and under p  
 A/Reference number: I53305; MUID:85179510; PMID:6241892  
 A/Accession: I53305  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1872-1933, 'I', 1935-1938 <RRS>  
 A/Cross-references: GB:M32697; NID:9205596; PIDN:AAA1658.1; PID:9205597  
 C/Superfamily: myosin heavy chain; myosin motor domain homology  
 C/Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl  
 F, 87-767/Domain: myosin motor domain homology <MMOT>  
 F, 177-184/Region: nucleotide-binding motif A (P-loop)  
 F, 548-585/Region: actin binding #status predicted  
 F, 656-678/Region: actin binding #status predicted  
 F, 840-1938/Domain: coiled coil #status predicted  
 F, 840-1280/Region: 82  
 F, 1281-1938/Region: light meromyosin  
 F, 128/Modified site: N6, N6, N6-trimethyllysine (lys) #status predicted  
 F, 183/Binding site: ATP (lys) #status predicted  
 F, 696, 706/Active site: Cys #status predicted

Query Match      39.7%;      Score 54;      DB 1;      Length 1938;  
 Best Local Similarity      50.0%;      Pred. No. 26;  
 Matches      10;      Conservative      3;      Mismatches      7;      Indels      0;      Gaps      0;

QY      2      RYTHPLPKDLYRSIAKAPG 21  
 DB      664      RTTHPFPVRCITPERRAPG 683

RESULT 11  
 A46762  
 myosin alpha heavy chain, cardiac muscle - human  
 N/Contains: myosin ATPase (EC 3.6.4.1)  
 C/Species: Homo sapiens (man)  
 C/Date: 31-Dec-1993 #sequence (revision 31-Dec-1993 #text\_change 09-Jul-2004  
 A/Accession: A46762; B46762; A49354; S18830; B32562; B33835; B27858; A28908  
 R/Matsuoka, R.; Beisel, K.W.; Funttani, M.; Arai, S.; Takao, A.  
 Am. J. Med. Genet. 41, 537-547, 1991  
 A/Title: Complete sequence of human cardiac alpha-myosin heavy chain gene and amino acid  
 A/Reference number: A46762; MUID:92133655; PMID:1776652  
 A/Accession: A46762  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: DNA  
 A/Residues: 1-1939 <MAT>  
 A/Cross-references: UNIPROT:P13533; UNIPROT:Q9UQV1; DBJ:DD00943; NID:9219523; PIDN:BAAO  
 A/Accession: B46762  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-1461 <MA2>  
 R/BP, T.A.; Dixon, I.M.C.; Wang, H.Y.; Sole, M.J.; Llew, C.C.  
 Genomics 18, 505-509, 1993  
 A/Title: Structural organization of the human cardiac alpha-myosin heavy chain gene (MYH  
 A/Reference number: A49354; MUID:94140346; PMID:8307559  
 A/Accession: A49354  
 A/Status: nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-87, 'Q', 89-573, 'Q', 575-607, 'A', 609-743, 'T', 745-789, 'W', 791-1013, 'V', 1015-10  
 A/Cross-references: GB:Z20656; NID:9297023; PIDN:CAA79675.1; PID:9297024  
 R/Brand, N.J.; Dabnadi, N.; Yacoub, M.; Barton, P.J.R.  
 Biochem. Biophys. Res. Commun. 179, 1255-1258, 1991  
 A/Title: Determination of the 5' exon structure of the human cardiac alpha-myosin heavy  
 A/Accession: S18830; MUID:92028859; PMID:1930170  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-32 <BRA>  
 A/Cross-references: EMBL:X56181; NID:928318; PIDN:CAA39642.1; PID:928319  
 R/Yamauchi-Takahara, K.; Sole, M.J.; Llew, C.C.; Ing, D.; Llew, C.C.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989  
 A/Title: Characterization of human cardiac myosin heavy chain genes.

A:Reference number: A34224; MUID:89264452; PMID:2726733  
A:Accession: B32562  
A:Molecule type: DNA  
A:Residues: 1-87, 'Q', 89-177, 1551-1732, 'E', 1734-1736, 'T', 1738-1762, 'D', 1764-1848 <YAL>  
R:Yamauchi-Takahara, K.; Sole, M.J.; Llew, J.; Ing, D.; Llew, C.C.  
Proc. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989  
A:Reference number: A94226  
A:Contents: erratum  
A:Accession: B33835  
A:Molecule type: DNA  
A:Residues: 1-87, 'Q', 89-177, 1551-1732, 'E', 1734-1736, 'T', 1738-1762, 'D', 1764-1939 <YAS>  
R:Saez, L.J.; Glanola, K.M.; McCall, E.M.; Peghall, R.; Eddy, R.; Shows, T.B.; Leinwand  
Nucleic Acids Res. 15, 5443-5459, 1987  
A>Title: Human cardiac myosin heavy chain genes and their linkage in the genome.  
A:Reference number: A53669; MUID:87260010; PMID:3037493  
A:Accession: B27858  
A:Molecule type: DNA  
A:Residues: 1-3, 'S', 5-10, 'T', 12, 14-67 <SAB>  
R:Kurabayashi, M.; Tsuchimochi, H.; Komuro, I.; Takaku, F.; Yazaki, Y.  
J. Clin. Invest. 82, 524-531, 1988  
A>Title: Molecular cloning and characterization of human cardiac alpha- and beta-form myosin actin.  
A:Reference number: A92770; MUID:88299163; PMID:2969919  
A:Accession: A28908  
A:Molecule type: mRNA  
A:Residues: 1407-1532, 'N', 1534-1539, 'W', 1541-1576, 'NV', 1579-1704, 'EQ', 1707-1762, 'D', 1764-1939  
A:Cross-references: GB:M2164; NID:G189006; PIDN:AA36344.1; PID:G386972  
A:Experimental source: fetal heart  
C:Genetics:  
A:Gene: GDB:MYH6  
A:Cross-references: GDB:120214; OMIM:160710  
A:Map position: 14q11.2-14q13  
C:Superfamily: myosin heavy chain; myosin motor domain homology  
C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methylase  
P:88-768/Domain: myosin motor domain homology <MMOT>  
P:178-185/Region: nucleotide-binding motif A (P-loop)  
P:548-566/Region: actin binding #status predicted  
P:657-679/Region: actin binding #status predicted  
P:841-1319/Domain: coiled coil #status predicted <COI>  
P:1282-1939/Region: 1800 meromyosin  
P:1129/Modified site: N6, N6, N6-trimethyllysine (lys) #status predicted  
P:184/Binding site: ATP (lys) #status predicted  
P:697, 707/Active site: Cys #status predicted

Query Match 39.7%; Score 54; DB 1; Length 1939;  
Best Local Similarity 50.0%; Pred. NO. 26;  
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

2 RVTGPHLPKDIVRSTAKAG 21  
|||||:|:|  
Db 665 RTTHPHFVRCITIPERKAG 684

RESULT 12  
148175  
myosin heavy chain alpha, cardiac muscle [similarity] - golden hamster  
C:Species: Mesocricetus auratus (golden hamster)  
C:Date: 02-Jul-1996 #sequence\_rev10n 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: 148175, A23338  
A:Accession: 148175, A23338  
R:Wang, R.; Sole, M.J.; Cukerman, E.; Llew, C.C.  
J. Mol. Cell. Cardiol. 26, 1155-1165, 1994  
A>Title: Characterization and nucleotide sequence of the cardiac alpha-myosin heavy chain  
A:Reference number: 148153; MUID:95115033; PMID:7815459  
A:Accession: 148175  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1939 <RES>  
A:Cross-references: UNIPROT:P13539; GB:U15351; NID:G402373; PIDN:AA59701.1; PID:G402374  
R:Llew, C.C.; Jandreski, M.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 3175-3179, 1986  
A>Title: Construction and characterization of the alpha-form of a cardiac myosin heavy c  
A:Reference number: A23938; MUID:86205859; PMID:3456174

```

A:Accession: A233938
A:Molecule type: mRNA
A:Residues: 1630-1843, 'R', 1845-1878, 'T', 1880-1927, 'N', 1929-1932, 1934-1939 <LIB>
C:Species:
C:Accession: 67/3; 115/3; 168/1; 177/2; 214/3; 245/3; 267/1; 300/1; 334/3; 381/1; 470/3;
392/3; 1453/3; 1509/1; 1550/3; 1653/3; 1721/3; 1763/3; 1855/3; 1887/3; 1932/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: ATP; cardiac muscle; heart; nucleotide binding; P-loop
F:188-768/Domain: myosin motor domain homology <MOT>
F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 39.7%; Score 54; DB 2; Length 1939;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 RVTNPHLPKDIVRSIAKAPG 21
DB 665 RTTHPHFVRCIIPERRAKPG 684

RESULT 13
B87319
hypothetical protein CC0564 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87319
R:Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Lab, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo-
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference numbers: A87249; MUID:21173698; PMID:11259647
A:Accession: B87319
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-273 <SDO>
A:Cross-references: UNIPROT:Q9AAN3; GB:AE005673; NID:G13421758; PIDN:AAK22550.1; GSPDB:
A:Gene: CC0564

Query Match 38.2%; Score 52; DB 2; Length 273;
Best Local Similarity 40.6%; Pred. No. 7;
Matches 13; Conservative 5; Mismatches 4; Indels 10; Gaps 2;

QY 4 THPHLP--KDIVRS-----IAKAPGKAP 25
DB 224 SRPHAPRNRIIRSTLRGRDKPLCARANGRRAP 255

RESULT 14
T35963
hypothetical protein SC9C7.12 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T35963
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21551
A:Accession: T35963
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-197 <SEB>
A:Cross-references: UNIPROT:Q9ZBJ6; EMBL:AL035161; PIDN:CAA22724.1; GSPDB:GN00070; SCOE
A:Experimental source: strain A3 (2)
C:Genetics:
A:Gene: SC0EDB:SC9C7.12

Query Match 37.5%; Score 51; DB 2; Length 197;
Best Local Similarity 42.9%; Pred. No. 7;
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 3 VTHPHLPKDIVRSIAKAPGR 23
: ||| : ||||: ||:|

```

Db 177 LAHPALQAAYRALARPQR 197

# RESULT 15

B46529  
Ig Y heavy chain (7.88) - duck  
N:Alternate names: Ig gamma chain (7.88)  
C:Species: Anas platyrhynchos (domestic duck)  
C>Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
C:Accession: B46529; S20759  
R:Magor, K.E.; Watt, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.  
J:Immunol. 149, 2627-2633, 1992  
A:Title: Structural relationship between the two Igy of the duck, Anas platyrhynchos: md  
A:Reference number: A46529; MUID:93017865; PMID:1401901  
A:Accession: B46529  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-572 <MAG>  
A:Cross-references: EMBL:X65219; NID:G62442; PIDN:CAA46322.1; PID:G62443  
A:Experimental source: spleen  
A>Note: sequence extracted from NCBI backbone (NCBI:P:116127)  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:37-120/Domain: immunoglobulin homology <IMM>

Query Match 37.5%; Score 51; DB 2; Length 572;  
Best Local Similarity 50.0%; Pred. No. 21;  
Matches 11; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

OY 1 CRVTHPHLPKDIYRSIAKPGK 22  
Db 442 CTVOHEDLPVPLGKSIKHAAGK 463

Search completed: February 22, 2005, 07:01:47  
Job time : 39 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 22, 2005, 06:39:23 / Search time 175 Seconds

(without alignments)  
73.154 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136  
Sequence: 1 CRVTHPLPDIVRSIAKARKRKP 25

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqe, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID        | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 105   | 77.2        | 429    | 1 EPC_RAT    | P01855 rattus norv |
| 2          | 86    | 63.2        | 428    | 1 EPC_HUMAN  | P01854 homo sapien |
| 3          | 80    | 58.8        | 421    | 1 EPC_MOUSE  | P06336 mus musculu |
| 4          | 59    | 43.4        | 684    | 2 Q90544     | Q90544 ginglymasto |
| 5          | 55    | 40.4        | 1080   | 2 Q61P25     | Q61P25 xenopus lae |
| 6          | 54    | 39.7        | 99     | 2 Q9MY65     | Q9MY65 oryctolagus |
| 7          | 54    | 39.7        | 1938   | 1 MYH6_RAT   | P02563 rattus norv |
| 8          | 54    | 39.7        | 1938   | 1 MYH6_HUMAN | P13533 homo sapien |
| 9          | 54    | 39.7        | 1939   | 1 MYH6_MESAU | P13539 mesocricetu |
| 10         | 53    | 39.0        | 538    | 2 Q7R2J3     | Q7R2J3 neurospora  |
| 11         | 53    | 39.0        | 906    | 2 Q870P3     | Q870P3 neurospora  |
| 12         | 52    | 38.2        | 273    | 2 Q9AAN3     | Q9AAN3 caulobacter |
| 13         | 51.5  | 37.9        | 466    | 2 Q6N096     | Q6N096 homo sapien |
| 14         | 51    | 37.5        | 197    | 2 Q9ZBR8     | Q9ZBR8 streptomyce |
| 15         | 51    | 37.5        | 1004   | 2 Q6BEP3     | Q6BEP3 mus musculu |
| 16         | 51    | 37.5        | 1935   | 2 Q6DIX8     | Q6DIX8 xenopus tro |
| 17         | 51    | 37.5        | 1938   | 1 MYH6_MOUSE | Q02566 mus musculu |
| 18         | 51    | 37.5        | 1940   | 1 MYH3_HUMAN | P11055 homo sapien |
| 19         | 51    | 37.5        | 1940   | 1 MYH3_RAT   | P12847 rattus norv |
| 20         | 50.5  | 37.1        | 223    | 2 Q8ZGJ2     | Q8ZGJ2 streptomyce |
| 21         | 50.5  | 37.1        | 327    | 1 GQ4_HUMAN  | P01861 homo sapien |
| 22         | 50.5  | 37.1        | 330    | 1 GQ4_MOUSE  | P01863 mus musculu |
| 23         | 50.5  | 37.1        | 399    | 1 GCAM_MOUSE | P01865 mus musculu |
| 24         | 50.5  | 37.1        | 473    | 1 Q8TC63     | Q8TC63 homo sapien |
| 25         | 50.5  | 37.1        | 476    | 2 Q6MZX7     | Q6MZX7 homo sapien |
| 26         | 50.5  | 37.1        | 538    | 2 Q9K9R8     | Q9K9R8 bacillus ha |
| 27         | 50    | 36.8        | 68     | 2 Q9UMR8     | Q9UMR8 homo sapien |
| 28         | 50    | 36.8        | 736    | 1 MYH7_RABIT | P04461 oryctolagus |
| 29         | 50    | 36.8        | 797    | 2 Q9T5U6     | Q9T5U6 felis silve |
| 30         | 50    | 36.8        | 1038   | 2 Q28699     | Q28699 oryctolagus |
| 31         | 50    | 36.8        | 1510   | 2 Q75186     | Q75186 oryza sativ |

|    |      |      |      |              |                     |
|----|------|------|------|--------------|---------------------|
| 32 | 50   | 36.8 | 1934 | 1 MYH7_MESAU | P13540 mesocricetu  |
| 33 | 50   | 36.8 | 1935 | 1 MYH7_HUMAN | P12883 homo sapien  |
| 34 | 50   | 36.8 | 1935 | 1 MYH7_PIG   | P79293 sus scrofa   |
| 35 | 50   | 36.8 | 1935 | 1 MYH7_RAT   | P02564 rattus norv  |
| 36 | 50   | 36.8 | 1935 | 2 Q8W0U9     | Q8W0U9 equus caball |
| 37 | 50   | 36.8 | 1935 | 2 Q9B839     | Q9B839 bos taurus   |
| 38 | 50   | 36.8 | 1935 | 2 Q9GKR1     | Q9GKR1 sus scrofa   |
| 39 | 50   | 36.8 | 1935 | 2 Q91Z83     | Q91Z83 mus musculu  |
| 40 | 49.5 | 36.4 | 336  | 1 GCB_MOUSE  | P01866 mus musculu  |
| 41 | 49.5 | 36.4 | 373  | 2 Q76LV9     | Q76LV9 mus musculu  |
| 42 | 49.5 | 36.4 | 374  | 1 SPOF_HUMAN | O43791 homo sapien  |
| 43 | 49.5 | 36.4 | 374  | 1 SPOF_MOUSE | Q62988 mus musculu  |
| 44 | 49.5 | 36.4 | 374  | 2 Q6P8B3     | Q6P8B3 xenopus tro  |
| 45 | 49.5 | 36.4 | 374  | 2 Q7ZX06     | Q7ZX06 xenopus lae  |

## ALIGNMENTS

```

RESULT 1
EPC_RAT
ID EPC_RAT STANDARD, PRT, 429 AA.
AC P01855;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig epsilon chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
RC STRAIN=LDU/C/MSL;
RX MEDLINE=83064537; PubMed=6292865;
RA Hellman L., Petersen U., Engstrom A., Karlsson T., Bennich H.;
RT "Structure and evolution of the heavy chain from rat immunoglobulin
   B.";
RL Nucleic Acids Res. 10:6041-6049(1982).
RN [2]
RP SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
RX MEDLINE=83182019; PubMed=6820340;
RA Kindsvogel W.R., Reddy B.P., Moore J.M., Faust C.H. Jr.;
RT "A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
   construction, identification, and DNA sequence.";
RL DNA 1:335-343(1982).
RN [3]
RP SEQUENCE OF 205-306 FROM N.A.
RX MEDLINE=82174576; PubMed=6803238;
RA Hellman L., Petersen U., Bennich H.;
RT "Characterization and molecular cloning of the mRNA for the heavy
   (epsilon) chain of rat immunoglobulin B.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
-- SIMILARITY: Contains 4 immunoglobulin-like domains.
-----
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CC EMBL, J00744; AAA41379.1; ALT_INIT.
CC PIR, A93442; EHRT.
CC HSSP, P01854; IFP5.
CC InterPro, IPR007110; Ig-like.
CC InterPro, IPR003597; Ig_c1.
CC InterPro, IPR003006; Ig_MHC.
CC Pfam, PF00047; Ig1_4.
CC SMART, SM00407; IgC1_1.
CC PROSITE, PS50835; IG_LIKE; 4.
CC PROSITE, PS00290; IG_MHC; 3.

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KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT NON_TER 1
FT DOMAIN 6
FT DOMAIN 103
FT DOMAIN 205
FT DOMAIN 314
FT DOMAIN 414
FT COMPACT 168
FT COMPACT 308
SQ SEQUENCE 429 AA; 46671 MW; D2970B34EP8A72B0 CRC64;

Query Match 7.28; Score 105; DB 1; Length 429;
Best Local Similarity 79.28; Pred. No. 7.9e-07;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CRVTHPLPDIVRSIAKAPGRKA 24
Db 289 CRVDHPFPKPIRSTITKAPGRKS 312

RESULT 2
ID EPC_HUMAN STANDARD; PRT; 428 AA.
AC P01854;
DT 21-JUL-1986 (Rel. 01. Created)
DT 21-JUL-1986 (Rel. 01. Last sequence update)
DT 25-OCT-2004 (Rel. 45. Last annotation update)
DE Ig epsilon chain C region.
GN Name:IGH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8316897; PubMed=6300763;
RA Kikuchi M., Kurokawa T., Ono Y., Onoda H., Sasada R., Igarashi K.,
RT "Molecular cloning and nucleotide sequencing of human immunoglobulin
RL epsilon chain cDNA."
RN Nucleic Acids Res. 11:719-726(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83001945; PubMed=6286268; DOI=10.1016/0092-8674(82)90185-4;
RA Max E.B., Battey J., Ney R., Kirsch I.R., Leder P.;
RT "Duplication and deletion in the human immunoglobulin epsilon genes."
RN Cell 29:691-699(1982).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236029; PubMed=6234164;
RA Flanagan J.G., Rabbitts T.H.;
RT "The sequence of a human immunoglobulin epsilon chain constant
RL region gene, and evidence for three non-allelic genes."
RN EMBO J. 1:655-660(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84207910; PubMed=6327276;
RA Ueda S., Nakai S., Nishida Y., Hisejima H., Honjo T.;
RT "Long terminal repeat-like elements flank a human immunoglobulin
RL epsilon pseudogene that lacks introns."
RN EMBO J. 1:1539-1544(1982).
RN [5]
RP PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
RA Benich H.H., Johanson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RT Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
RN [6]
RP SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.
RX MEDLINE=83065234; PubMed=6815556;
RA Keren J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RL Bell L.O., Gould H.O.;
RT "Cloning and sequence determination of the gene for the human
RL immunoglobulin epsilon chain expressed in a myeloma cell line."

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RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [7]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=87089848; PubMed=3796618; DOI=10.1016/0161-5890(86)90005-2;
RA Padlan E.A., Davies D.R.;
RT "A model of the Fc of immunoglobulin E."
RL Mol. Immunol. 23:1063-1075(1986).
CC -1- SIMILARITY: Contains 4 immunoglobulin-like domains.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, L00022; AAB59424.1; ALT_INIT.
DR PIR, A22771; EHHU.
DR PDB, 1F6A; X-ray; B/D=207-428.
DR PDB, 1F65; X-ray; A=207-428.
DR PDB, 1G84; NMR; A=106-210.
DR PDB, 1IGR; Model; A/B=-.
DR PDB, 1OOV; X-ray; A/B=102-428.
DR Genew; HGNC:5522; IGHE.
DR MIM, 147180; -.
DR GO, GO:0003823; F:antigen binding; NAS.
DR GO, GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-1like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00407; Ig1; 4.
DR SMART; SM00407; IGcl; 4.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW 3D-structure; Direct protein sequencing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT NON_TER 1
FT DOMAIN 1
FT DOMAIN 6
FT DOMAIN 112
FT DOMAIN 210
FT DOMAIN 214
FT DOMAIN 318
FT DOMAIN 324
FT DISULFID 14
FT DISULFID 15
FT DISULFID 105
FT DISULFID 29
FT DISULFID 85
FT DISULFID 121
FT DISULFID 121
FT DISULFID 135
FT DISULFID 193
FT DISULFID 209
FT DISULFID 239
FT DISULFID 239
FT DISULFID 345
FT CARBOHYD 21
FT CARBOHYD 49
FT CARBOHYD 99
FT CARBOHYD 146
FT CARBOHYD 146
FT CARBOHYD 252
FT CARBOHYD 252
FT CARBOHYD 275
FT VARIANT 359
FT STRAND 113
FT STRAND 119
FT STRAND 130
FT STRAND 138
FT STRAND 148
FT TURIN 151
FT STRAND 152
FT STRAND 153
FT STRAND 154
FT HELIX 156
FT STRAND 158
FT STRAND 160
FT STRAND 165
FT STRAND 163
FT STRAND 173
FT HELIX 181
FT STRAND 182
FT TURIN 187
FT STRAND 188
FT STRAND 191
FT STRAND 201
FT STRAND 206
FT STRAND 218
FT HELIX 221
FT HELIX 226
FT TURIN 230
FT TURIN 232

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CC EMBL; X01857; CAA25977.1; -.
CC EMBL; X01857; CAA25978.1; -.
CC PIR; A02144; EHMS.
CC HSSP; P01854; IEP5.
CC DR InterPro; IPR007110; Ig_1like.
CC DR InterPro; IPR003597; Ig_c1.
CC DR InterPro; IPR003006; Ig_MHC.
CC PIR; P00047; Ig; 4.
CC DR SMART; SMO0407; IGC1; 2.
CC DR PROSITE; PS50835; IG_LIKB; 4.
CC DR PROSITE; PS00290; IG_MHC; 3.
CC Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.
CC FT NOK_TER 1 1
CC FT DOMAIN 1 90 CH1.
CC FT DOMAIN 91 197 CH2.
CC FT DOMAIN 198 304 CH3.
CC FT DOMAIN 305 421 CH4.
CC FT DISULFID 23 75 By similarity.
CC FT DISULFID 121 180 By similarity.
CC FT DISULFID 226 285 By similarity.
CC FT DISULFID 330 392 By similarity.
CC FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 72 72 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 84 84 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 95 95 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 166 166 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 238 238 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 365 365 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 415 415 N-linked (GlcNAc...) (Potential).
CC SO SEQUENCE 421 AA; 47320 MW; 8F909E1F30A06B47 CRC64;
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\Qy 1 CRVTHPHLPDPIYRSIAKAPGKRA 24
Db 285 CIVDHPDPFKPIYRSITKTEGQSS 308
Matches 15; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
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RESULT 4
Q90544 PRELIMINARY; PRT; 684 AA.
ID O90544
AC O90544;
DT 01-NOV-1996 (TRENBLREL.01, Created)
DT 01-NOV-1996 (TRENBLREL.01, Last sequence update)
DT 01-MAR-2004 (TRENBLREL.26, Last annotation update)
DT Novel antigen receptor precursor.
OS Ginglymostoma cirratum (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC Ginglymostomatidae; Ginglymostoma.
OX NCBI_TaxID=7801;
RX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MERRILLE-95183140; PubMed=7877689; DOI=10.1038/374168a0;
RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks.";
RL Nature 374:168-173(1995).
DR EMBL; U18701; AAB48195.1; -.
DR PIR; S60266; S60266.
DR HSSP; P01842; IAOK.
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DR GO:0004872; F:receptor activity; IEA.  
 DR Pfam; PF07654; Cl-act; 3.  
 DR SMART; SM00047; Ig; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MEC; UNKNOWN\_3.  
 DR Receptor; Signal.  
 FT SIGNAL 1 18 Potential  
 FT CHAIN 19 684 novel antigen receptor.  
 SQ SEQUENCE 684 AA; 75224 MW; 2F9D2071CD456FD CRC64;

Query Match 43.4%; Score 59; DB 2; Length 684;  
 Best Local Similarity 50.0%; Pred. No. 7.4;  
 Matches 11; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRVTHPLPDIVRSIAKAPG 22  
 Db 645 CLVGHPSLRDLIRSNKNGK 666

RESULT 5  
 ID Q6IP25 PRELIMINARY; PRT; 1080 AA.  
 AC Q6IP25;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE LOC332141 protein (Fragment).  
 GN Name=LOC332141;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesodactylia; Pipidea; Pipidae;  
 OC Xenopodidae; Xenopus.  
 CX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Hopsch S.F., Zeeberg B., Buettow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide P.,  
 RA DiCicco L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Frange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
 RA Richards S., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
 RA Pabey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakeley M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalka U., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.,  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative.";  
 RT Dev. Dyn. 225:384-391 (2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RA Klein S., Strausberg R.,  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DB EMBL, BC072094; AAT72094.1; -.

DR HSPB; P24733; 1KK8.  
 DR GO:0016459; C:myosin; IEA.  
 DR GO:0005524; F:ATP binding; IEA.  
 DR GO:0003774; F:motor activity; IEA.  
 DR InterPro; IPR000048; IQ region.  
 DR InterPro; IPR001609; Myosin head.  
 DR InterPro; IPR004009; Myosin\_N.  
 DR Pfam; PF00612; IQ; 2.  
 DR Pfam; PF00063; Myosin\_head; 1.  
 DR Pfam; PF02736; Myosin\_N; 1.  
 DR PRINTS; PR00193; MYOSINHEAVY.  
 DR Prodom; PD000355; Myosin\_head; 1.  
 DR SMART; SM00015; IQ; 2.  
 DR SMART; SM00242; MYSC; 1.  
 DR PROSITE; PS50996; IQ; 1.  
 FT NON\_TER 1080  
 SQ SEQUENCE 1080 AA; 123936 MW; 5BDC6234B598B9F5 CRC64;

Query Match 40.4%; Score 55; DB 2; Length 1080;  
 Best Local Similarity 47.6%; Pred. No. 46;  
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 RYTHPLPDIVRSIAKAPG 22  
 Db 660 RTTHPFPVRCIIPNERKAPG 680

RESULT 6  
 ID Q9MY55 PRELIMINARY; PRT; 99 AA.  
 AC Q9MY55;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Myosin heavy chain (Fragment).  
 GN Name=myh6;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 CX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=New Zealand White; TISSUE=Heart;  
 RA Sayed R.A., Grace A.A., Vandenberg J.I.,  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ291317; CAB94849.1; -.  
 DR HSPB; P13538; 2MTS.  
 DR GO:0016459; C:myosin; IEA.  
 DR GO:0005524; F:ATP binding; IEA.  
 DR GO:0003774; F:motor activity; IEA.  
 DR InterPro; IPR001609; Myosin\_head.  
 DR Pfam; PF00063; Myosin\_head; 1.  
 FT NON\_TER 99  
 SQ SEQUENCE 99 AA; 10933 MW; 3961CA1047DB2B0C CRC64;

Query Match 39.7%; Score 54; DB 2; Length 99;  
 Best Local Similarity 50.0%; Pred. No. 5.5;  
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 RYTHPLPDIVRSIAKAPG 21  
 Db 79 RTTHPFPVRCIIPNERKAPG 98

RESULT 7  
 ID MYH6\_RAT STANDARD; PRT; 1938 AA.  
 AC P02563; Q63351;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).

GN Name=Myh6;  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=90016822; PubMed=2798111;  
 RA Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;  
 RT "Complete nucleotide sequence of full length cDNA for rat alpha  
 RT cardiac myosin heavy chain.";  
 RL Nucleic Acids Res. 17:7527-7528(1989).  
 RN [2]  
 RP DISCUSSION OF SEQUENCE.  
 RX MEDLINE=9013319; PubMed=2614840;  
 RA McNeill E.M., Kraft R., Bravo-Zehnder M., Taylor D., Leinwand L.A.;  
 RT "Full-length rat alpha and beta cardiac myosin heavy chain sequences.  
 RT Comparisons suggest a molecular basis for functional differences.";  
 RL J. Mol. Biol. 210:665-671(1989).  
 RN [3]  
 RP SEQUENCE OF 1-167 FROM N.A.  
 RX MEDLINE=84194059; PubMed=5585819;  
 RA Mahdavi V., Chambers A.P., Nadal-Ginard B.;  
 RT "Cardiac alpha- and beta-myosin heavy chain genes are organized in  
 RT tandem.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2626-2630(1984).  
 RN [4]  
 RP SEQUENCE OF 1512-1938 FROM N.A.  
 RX MEDLINE=8220036; PubMed=7045682;  
 RA Mahdavi V., Perlasamy M., Nadal-Ginard B.;  
 RT "Molecular characterization of two myosin heavy chain genes expressed  
 RT in the adult heart.";  
 RL Nature 297:659-664(1982).  
 RN [5]  
 RP SEQUENCE OF 1872-1938 FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RX MEDLINE=85179510; PubMed=6241892;  
 RA Mahdavi V., Lompre A.M., Chambers A.P., Nadal-Ginard B.;  
 RT "Cardiac myosin heavy chain isozytic transitions during development  
 RT and under pathological conditions are regulated at the level of mRNA  
 RT availability.";  
 RL Eur. Heart J. 5:181-191(1984).  
 CC -1- FUNCTION: Muscle contraction.  
 CC -1- SUBUNIT: Myosin is a hexameric protein that consists of 2  
 CC heavy chain subunits (MHC), 2 alkali light chain subunits (MLC)  
 CC and 2 regulatory light chain subunits (MLC-2).  
 CC -1- DOMAIN: The rodlike tail sequence is highly repetitive, showing  
 CC cycles of a 28-residue repeat pattern composed of 4 heptapeptides,  
 CC characteristic for alpha-helical coiled coils.  
 CC -1- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light  
 CC meromyosin (MM) and 1 heavy meromyosin (HMM). It can later be  
 CC split further into 2 globular subfragments (S1) and 1 rod-shaped  
 CC subfragment (S2).  
 CC -1- MISCELLANEOUS: The cardiac alpha isoform is a 'fast' ATPase  
 CC myosin, while the beta isoform is a 'slow' ATPase.  
 CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.  
 CC -----  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 CC EMBL: X15938; CAA34064.1; -  
 DR EMBL: K01464; AAA41648.1; -  
 DR EMBL: J00751; AAA41653.1; -  
 DR EMBL: M32697; AAA41658.1; -  
 DR PIR: S06005; S06005.

DR HSSP; P24733; IKOM.  
 DR RGD; 62029; Myh6.  
 DR InterPro; IPR000048; IQ\_region.  
 DR InterPro; IPR001609; Myosin\_head.  
 DR InterPro; IPR004009; Myosin\_N.  
 DR InterPro; IPR002928; Myosin\_tail.  
 DR Pfam; PF00642; IQ\_2.  
 DR Pfam; PF00653; Myosin\_head; 1.  
 DR Pfam; PF02736; Myosin\_N; 1.  
 DR Pfam; PF01576; Myosin\_tail; 1.  
 DR PRINTS; PR00193; MYOSINHEAVY.  
 DR ProDom; PD000355; Myosin\_head; 1.  
 DR PROSITE; PS50096; IQ; 1.  
 KW Actin-binding; ATP-binding; Calmodulin-binding; Coiled coil;  
 KW Myosin-binding; Multigene family; Muscle protein; Myosin; Thick filament.  
 FT DOMAIN 1  
 FT 782 811  
 FT 842 1938  
 FT 177 184  
 FT NP BIND 656 678  
 FT DOMAIN 758 772  
 FT 789 806  
 FT 815 832  
 FT 128 128  
 FT MOD RES 13 13  
 FT CONFLICT 46 46  
 FT CONFLICT 51 52  
 FT CONFLICT 87 87  
 FT CONFLICT 109 109  
 FT CONFLICT 1566 1566  
 FT CONFLICT 1575 1575  
 FT CONFLICT 1721 1721  
 FT CONFLICT 1852 1852  
 FT CONFLICT 1870 1870  
 FT CONFLICT 1934 1934  
 SQ SEQUENCE 1938 AA; 223507 MW; D7BD33FC2B19E3C2 CRC64;  
 Query Match 39.7%; Score 54; DB 1; Length 1938;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
 Cy 2 RVTHPHLPDVIYSIAKAPG 21  
 Db 664 KTHPHFVACIPNERKAPG 683  
 ID MYH6\_HUMAN STANDARD; PRT; 1939 AA.  
 AC P13533; Q13943; Q14906; Q14907;  
 DT 01-JUN-1990 (Rel. 13, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Myosin heavy chain, cardiac muscle alpha isoform (MYHC-alpha).  
 GN Name=Myh6; Synonyms=MYHCA;  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92133665; PubMed=1776652;  
 RA Matsuo K., Beisel K.W., Furutani M., Arai S., Takao A.;  
 RT "Complete sequence of human cardiac alpha-myosin heavy chain gene and  
 RT amino acid comparison to other myosins based on structural and  
 RT functional differences.";  
 RL Am. J. Med. Genet. 41:537-547(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94140346; PubMed=8307559;  
 RA Bep T.A., Dixon I.M., Wang H.Y., Sole M.J., Llew C.-C.;  
 RT "Structural organization of the human cardiac alpha-myosin heavy chain  
 RT gene (MYH6).";

Genomics 18:505-509(1993).  
 (3) SEQUENCE OF 1-177 AND 1551-1939 FROM N.A.  
 RA MEDLINE=89264452; PubMed=2726733.  
 RA Yamauchi-Takahara K., Sole M.J., Llew J., Ing D., Llew C.-C.,  
 RA "Characterization of human cardiac myosin heavy chain genes.",  
 RA Proc. Natl. Acad. Sci. U.S.A. 86:3504-3508(1989).  
 RA ERRATUM  
 RA Yamauchi-Takahara K., Sole M.J., Llew J., Ing D., Llew C.-C.,  
 RA Proc. Natl. Acad. Sci. U.S.A. 86:7416-7417(1989).  
 RA [5] SEQUENCE OF 1407-1939 FROM N.A.  
 RA MEDLINE=89299163; PubMed=2969919.  
 RA Kuriyama M., Tsuchimoto H., Komuro I., Takaku F., Yazaki Y.,  
 RA "Molecular cloning and characterization of human cardiac alpha-  
 RT beta-form myosin heavy chain complementary DNA clones. Regulation of  
 RT expression during development and characterization of human cardiac alpha-  
 RT U. Clin. Invest. 82:524-531(1988).  
 CC -1- FUNCTION: Muscle contraction.  
 CC -1- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2  
 CC heavy chain subunits (MHC) and 2 regulatory subunits (RLC).  
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.  
 CC cycles of a 28-residue repeat sequence is highly repetitive, showing  
 CC characteristic for alpha-helical pattern composed of 4 heptapeptides,  
 CC meromyosin (MM) and 1 heavy meromyosin (HMM). It can later be  
 CC split further into 2 globular subfragments (S1) and 1 rod-shaped  
 CC -1- MYOSIN: The cardiac alpha isoform is a 'fast' ATPase.  
 CC -1- SIMILARITY: Contains 1 IQ domain.  
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 CC or send an email to license@isb-sib.ch).  
 CC EMBL: D00943; BAB00791.1; -  
 CC EMBL: M20656; CAA7675.1; -  
 CC EMBL: M25142; AAA60386.1; -  
 CC EMBL: M25142; AAA60386.1; -  
 CC EMBL: M25141; AAA60387.1; -  
 CC EMBL: M25141; AAA60387.1; -  
 CC PIR: A46762; A46762.1; JOINED.  
 CC HSSP: P34732; A46762.1; -  
 CC GeneW: H4733; IKOM.  
 CC MIM: 160710; -  
 CC GO: GO:0005859; C:myosin myosin, NAS.  
 CC GO: GO:0005779; F:ATP binding, NAS.  
 CC GO: GO:0005524; F:ATP binding, NAS.  
 CC GO: GO:0005516; F:calcium binding, NAS.  
 CC GO: GO:0000466; P:myosin binding, NAS.  
 CC InterPro: IPR000048; IQ region  
 CC InterPro: IPR001609; Myosin head.  
 CC InterPro: IPR004009; Myosin head.  
 CC Pfam: PF006412; IQ\_2 Myosin head.  
 CC Pfam: PF006412; IQ\_2 Myosin head.  
 CC Pfam: PF02765; Myosin head, 1.  
 CC Pfam: PF02765; Myosin head, 1.  
 CC PRINTS: PR00193; Myosin head, 1.  
 CC PRINTS: PR00193; Myosin head, 1.  
 CC PROSITE: PS50096; Myosin head, 1.  
 CC Actin-binding; ATP-binding; Calmodulin-binding; Coiled coil;

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Page

Query Match 10; Similarity 39.7%; Score 54; DB 1; Length 1939;  
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0.  
 Db 2 RTTHPRLPNDIVYSAKAPG 21  
 665 RTTHPRLPNDIVYSAKAPG 684  
 ID MYH6 MESAU STANDARD; PRT; 1939 AA.  
 AC 013539; 060562;  
 DT 15-DEC-1998 (Rel. 13, Created)  
 DT 05-DEC-1998 (Rel. 37, Last sequence update)  
 GN Myosin heavy chain, cardiac muscle (update)  
 OS Mesocricetus auratus (Golden hamster).  
 CC Mesocricetus auratus (Golden hamster).  
 CC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OX NCBI TaxID=10036;  
 CC [1] TaxID=10036;  
 CC SEQUENCE FROM N.A.  
 CC STRAIN: FVB; TIGSD=J4ever;  
 CC MEDLINE=95115033; PubMed=7815455; DOI=10.1006/jmcc.1994.1134;  
 CC Wang R., Sole M.J., Llew J., Ing D., Llew C.-C.,  
 CC "Characterization of human cardiac myosin heavy chain complementary  
 CC U. Mol. Cell. Cardiol. 26:1155-1165(1994).  
 CC SEQUENCE OF 1630-1939 FROM N.A.  
 CC MEDLINE=86205859; PubMed=3458174;  
 CC Llew C.-C., Jandreski M.A.,  
 CC "Construction and characterization of the alpha form of a cardiac  
 CC Syrian hamster myosin heavy chain cDNA clone and its developmental expression in the  
 CC Proc. Natl. Acad. Sci. U.S.A. 83 3175-3179(1986)  
 CC -1- FUNCTION: Muscle contraction

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CC -1- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2
CC heavy chain subunits (MHC), 2 alkali light chain subunits (MLC)
CC and 2 regulatory light chain subunits (MLC-2).
CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibril.
CC -1- DOMAIN: The rodlike tail sequence is highly repetitive, showing
CC cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
CC characteristic for alpha-helical coiled coils.
CC -1- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light
CC meromyosin (LM) and 1 heavy meromyosin (HMM). It can later be
CC split further into 2 globular subfragments (S1) and 1 rod-shaped
CC subfragment (S2).
CC -1- MISCELLANEOUS: The cardiac alpha isoform is a 'fast' ATPase
CC myosin, while the beta isoform is a 'slow' ATPase.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L15351; AAB59701.1; -
DR EMBL: M12995; AAA37081.1; -
DR PIR: I48175; I48175.
DR HSSP: P24733; 1KQM.
DR InterPro: IPR0000048; IQ region.
DR InterPro: IPR001609; Myosin head.
DR InterPro: IPR004009; Myosin N.
DR InterPro: IPR002928; Myosin tail.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; Myosin head; 1.
DR Pfam: PF02736; Myosin N; 1.
DR Pfam: PF01576; Myosin tail 1; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; Myosin_head; 1.
DR PROSITE: PS50096; IQ; 1.
KW Actin-binding; ATP-binding; Calmodulin-binding; Coiled coil;
KW Myofibril; Multigene family; Muscle protein; Myosin; Thick filament.
FT DOMAIN 1 782 812
FT DOMAIN 842 1939
FT DOMAIN 1439 1443
FT NP BIND 178 185
FT DOMAIN 657 679
FT DOMAIN 759 773
FT MOD RES 129 129
FT CONFLICT 1633 1633
FT CONFLICT 1651 1651
FT CONFLICT 1686 1687
FT CONFLICT 1693 1693
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FT CONFLICT 1879 1879
FT CONFLICT 1885 1885
FT CONFLICT 1907 1907
FT CONFLICT 1928 1928
FT CONFLICT 1933 1935
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Query Match 39.7%; Score 54; DB 1; Length 1939;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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Db 665 RTTHPFLPKDVRISIAKAPG 21  
665 RTTHPFLPKDVRISIAKAPG 684

RESULT 10  
Q7RZJ3 PRELIMINARY; PRT; 538 AA.

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AC Q7RZJ3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU04012.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxId=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74X;
RA Galagan J.E., Calvo S.B., Borkovich K.A., Selker B.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Wang L.-J., Smirnov S., Putcuk E., Reiman B.,
RA Elkins T., Engels R., Ma S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Maeburne M.,
RA Saiteremikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Greer S.,
RA Kamal M., Kamyshele M., Mauceli E., Bielke C., Rudd S., Friedman D.,
RA Krysstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmann S.A.,
RA DeSouza C.C., Glass I., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seltzer S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Eboole D.J., Frettag M.,
RA Paulsen I., Sachs M.S., Lander B.S., Nussbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX01000718; EAA28391.1; -
DR EMBL: AABX01000718; EAA28391.1; -
SQ SEQUENCE 538 AA; 61419 MW; 6C98D237618739B4 CRC64;

Query Match 39.0%; Score 53; DB 2; Length 538;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

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Db 122 CRATPGLMKRIDDTAKGPFK 143

RESULT 11  
Q870P3 PRELIMINARY; PRT; 906 AA.  
ID Q870P3;  
AC Q870P3;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein 49D12.100.  
GN Name=49D12.100;  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
OX NCBI\_TaxId=5141;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Schulte U., Algen V., Hobeisel J., Brandt P., Fartmann B., Holland R.,  
RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA German Neurospora genome project;  
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BX295540; CAD79685.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 906 AA; 102137 MW; 71ED849AF8B03146 CRC64;

Query Match 39.0%; Score 53; DB 2; Length 906;  
Best Local Similarity 50.0%; Pred. No. 76;  
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRS-TAKAPGK 22  
DB 122 CRAFTPGMKRIDDYAKGPFK 143

## RESULT 12

Q9AAN3 PRELIMINARY; PRT; 273 AA.

DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein CC0564.  
GN OrderedLocustNames=CC0564.  
OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;  
OC Caulobacteraceae; Caulobacter.  
OX NCBI\_TaxId=155892;  
RN [1]

## SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;  
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298,  
RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
RA Porocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Hatt D.H.,  
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,  
RA Berry K.J., Uteback T.R., Tran K., Wolf A.M., Vamathevan J.J.,  
RA Ermlaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,  
RA Fraser C.M.,  
RT "Complete genome sequence of Caulobacter crescentus."  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
DR EMBL; AE005730; AAK2550.1; -.  
DR PIR; B87319; B87319.  
KW Complete proteome; Hypothetical protein.

QY SEQUENCE 273 AA; 29461 MW; C1C6D2F87E432082 CRC64;

Query Match 38.2%; Score 52; DB 2; Length 273;  
Best Local Similarity 40.6%; Pred. No. 31;

Matches 13; Conservative 5; Mismatches 4; Indels 10; Gaps 2;

QY 4 THPHLP-KDIVRS-----TAKAPGRAP 25  
DB 224 SRPHAPNRDIIIRSTLCGRKPLCARANGRRAP 255

## RESULT 13

Q6N096 PRELIMINARY; PRT; 466 AA.

DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686115196.  
GN Name=DKFZp686115196;  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]

## SEQUENCE FROM N.A.

RC TISSUE=Human esophagus tumor;  
RG The German Human CDNA Consortium;  
RG Wamutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,  
RA Fobo G., Han M., Wiemann S.,  
RL Submitted (Aug-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BX640620; CAB45774.1; -.  
DR HSS; P01861; IADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG\_1like.  
DR InterPro; IPR003597; IG\_c1.

DR InterPro; IPR00306; IG\_MHC.

DR InterPro; IPR003596; IG\_v.

DR Pfam; PF07554; C1-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGc1; 3.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG\_LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

KW Hypothetical protein.

QY SEQUENCE 466 AA; 50926 MW; 01E91B74BD6D57C4 CRC64;

## Query Match

Best Local Similarity 37.9%; Score 51.5; DB 2; Length 466;  
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 CRVTHPLPKDIVRS-TAKAPGK-RAP 25  
DB 340 CRVSNALPAPLEKTIISAKGQPREP 365

## RESULT 14

Q9ZBJ8 PRELIMINARY; PRT; 197 AA.

DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein SC06476.  
GN ORFNames=SC9C7.12;  
OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxId=1902;  
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M145;  
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-W., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kiebler H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,  
RA Huang C.-H., Kiebler T., Larke L., Murphy L.D., Oliver K., O'Neill S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Ruter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.,  
RT "Complete genome sequence of the model actinomycete Streptomyces

coelicolor A3(2)."

RL Nature 417:141-147(2002).

DR EMBL; AL939127; CAA22724.1; -.  
DR PIR; T35963; T35963.

DR InterPro; IPR008938; ARM.

DR InterPro; IPR004155; PBS\_lyase\_HEAT.

DR Pfam; PF03130; HEAT\_PBS; 1.

DR SMART; SM00567; EZ\_HEAT; 4.

KW Complete proteome; Hypothetical protein.

QY SEQUENCE 197 AA; 21061 MW; 6AB3643C5570AC1 CRC64;

QY 3 VTHPHLPKDIVRS-TAKAPGR 23  
DB 177 LAHPALAAVRLARIPGR 197

## RESULT 15

Q6P8P3 PRELIMINARY; PRT; 1004 AA.

AC Q6P8P3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)



DT 05-JUN-2004 (TrEMBLrel. 27, Last annotation update)  
DE Myh6 protein (Fragment).  
GN Name=Myh6;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung and heart;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueidi T.B., Toshlyuk S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung and heart;  
RA Strausberg R.;  
RL Submitted (NCV-2003) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC061145; AAH61145.1; -  
DR HSP, P24733; IKK8.  
DR GO; GO:0007522; P:visceral muscle development; IMP.  
DR InterPro; IPR000048; IQ\_region.  
DR InterPro; IPR001609; Myosin\_head.  
DR InterPro; IPR004009; Myosin\_N.  
DR Pfam; PF00612; IQ; 2.  
DR Pfam; PF00063; Myosin\_head; 1.  
DR Pfam; PF02736; Myosin\_N; 1.  
DR PRINTS; PR00193; MYOSINHEAVY.  
DR ProDom; PD000355; Myosin\_head; 1.  
DR SMART; SM00242; MYSC; 1.  
DR PROSITE; PSS0096; IQ; 1.  
FT NON\_TER 1004  
SQ SEQUENCE 1004 AA, 115137 MW, 0D8457AF2451F6EB CRC64,  
Query March 37.5%; Score 51; DB 2; Length 1004;  
Best Local Similarity 45.0%; Pred. No. 1.7e+02;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
CY 2 RVTHPHLPKDIIVRSIAKAPG 21  
: ||||| : : : |||||  
Db 665 KTHPHFVRCIIIPNERRAPG 684

Search completed: February 22, 2005, 07:00:16  
Job time : 177 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 22, 2005, 07:11:31, Search time 38 Seconds  
(without alignments)  
63.301 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDLYRSIAKAPGRAP 25

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4989

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: 1: PIR 79:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 29    | 21.3        | 25     | 2 S07770 | histone H2B.1, spe |
| 2          | 28    | 20.6        | 11     | 2 S78765 | ribosomal protein  |
| 3          | 27    | 19.9        | 16     | 2 P11351 | ig heavy chain DJ  |
| 4          | 27    | 19.9        | 20     | 2 A41439 | acid ribonuclease  |
| 5          | 27    | 19.9        | 25     | 1 Z1BPG4 | gene J protein - p |
| 6          | 26.5  | 19.5        | 20     | 2 A36016 | granulocyte inhibi |
| 7          | 26.5  | 19.5        | 22     | 2 P00143 | polygalacturonase  |
| 8          | 26    | 19.1        | 13     | 2 S32551 | glutathione transf |
| 9          | 26    | 19.1        | 15     | 4 J38336 | hypothetical TBL/M |
| 10         | 26    | 19.1        | 20     | 2 JF0055 | ribosomal protein  |
| 11         | 26    | 19.1        | 22     | 2 H30608 | ig kappa chain V-I |
| 12         | 26    | 19.1        | 22     | 2 D30609 | ig kappa chain V-I |
| 13         | 26    | 19.1        | 24     | 2 B30609 | ig kappa chain V-I |
| 14         | 26    | 19.1        | 24     | 2 JF0052 | ribosomal protein  |
| 15         | 25    | 18.4        | 10     | 2 H37196 | bradykinin-potentl |
| 16         | 25    | 18.4        | 15     | 2 PA0071 | superoxide dismuta |
| 17         | 25    | 18.4        | 15     | 2 I50503 | agrin - electric r |
| 18         | 25    | 18.4        | 17     | 2 D22595 | bombolitin IV - Am |
| 19         | 25    | 18.4        | 20     | 2 F80028 | flagellar motor sw |
| 20         | 25    | 18.4        | 20     | 2 H28949 | ribosomal protein  |
| 21         | 25    | 18.4        | 21     | 2 B33600 | glutamate-ammoma   |
| 22         | 25    | 18.4        | 22     | 2 D47256 | kineoplast DNA-as  |
| 23         | 25    | 18.4        | 24     | 2 G85602 | hypothetical prote |
| 24         | 25    | 18.4        | 25     | 2 A60621 | hematocytin - Acti |
| 25         | 24    | 17.6        | 10     | 2 B37196 | bradykinin-potentl |
| 26         | 24    | 17.6        | 20     | 2 S23981 | outer layer protei |
| 27         | 24    | 17.6        | 20     | 2 S46479 | retinoid-X-recepto |
| 28         | 24    | 17.6        | 21     | 2 S51066 | ribosomal protein  |
| 29         | 24    | 17.6        | 22     | 2 C42856 | hypothetical prote |

|    |      |      |    |          |                    |
|----|------|------|----|----------|--------------------|
| 30 | 24   | 17.6 | 22 | 2 S42567 | cytochrome-b5 redu |
| 31 | 23.5 | 17.3 | 23 | 2 P50273 | hypothetical prote |
| 32 | 23.5 | 17.3 | 23 | 2 A41263 | kinase-related tra |
| 33 | 23   | 16.9 | 10 | 2 S77990 | cytochrome-c oxida |
| 34 | 23   | 16.9 | 15 | 2 B39109 | hypothetical 1.5K  |
| 35 | 23   | 16.9 | 16 | 2 P11317 | ig heavy chain DJ  |
| 36 | 23   | 16.9 | 16 | 2 S65709 | major allergen Myr |
| 37 | 23   | 16.9 | 18 | 2 B27504 | histone H2B - mous |
| 38 | 23   | 16.9 | 19 | 2 PA0012 | superoxide dismuta |
| 39 | 23   | 16.9 | 20 | 2 S09025 | carboxylesterase ( |
| 40 | 23   | 16.9 | 20 | 2 A42865 | Ca2+/calmodulin-de |
| 41 | 23   | 16.9 | 21 | 2 S57568 | T cell receptor V- |
| 42 | 23   | 16.9 | 22 | 2 C48186 | ATPase R1 subunit  |
| 43 | 23   | 16.9 | 23 | 2 S23518 | ectomelysin (EC 3. |
| 44 | 23   | 16.9 | 23 | 2 S72535 | probable acr-2 reg |
| 45 | 22   | 16.2 | 7  | 2 A44428 | platelet aggregati |

#### ALIGNMENTS

```

RESULT 1
S07770
histone H2B.1, sperm - sea urchin (Echinus esculentus) (fragment)
C:Species: Echinus esculentus
C>Date: 30-Sep-1991 #sequence_rev: 30-Sep-1991 #text_change 09-Jul-2004
R:Accession: S07770
R:Hit: C.S./Thomas, J.O.
Eur. J. Biochem. 187, 145-153, 1990
A>Title: Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal ta
A:Reference number: S07769; PMID:90126812; PMID:2298202
A:Accession: S07770
A:Molecule type: protein
A:Residues: 1-25 <HIL>
A:Cross-references: UNIPROT:P13281
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 21.3%; Score 29; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 18 KAPGRAP 25
DB 4 KSPTKSP 11

RESULT 2
S78765
ribosomal protein MRP-524, mitochondrial - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Sep-1999 #sequence_rev: 20-Sep-1999 #text_change 09-Jul-2004
R:Accession: S78765
R:Hit: Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78765
A:Molecule type: protein
A:Residues: 1-11 <GRA>
A:Cross-references: UNIPROT:Q7M374
C:Keywords: mitochondrial
P:1-11/Product: ribosomal protein MRP-524 (fragment) #status experimental <MAT>

Query Match 20.6%; Score 28; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 HPLPKDLYR 14
DB 2 HVDVPRDLTK 11

RESULT 3

```

PH1351  
 Ig heavy chain DJ region (clone C100-109B) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C/Accession: PH1351  
 R/Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma  
 A/Reference number: PH1302; MUID:93094761; PMID:1460419  
 C/Accession: PH1351  
 A/Molecule type: DNA  
 A/Residues: 1-16 <NMS>  
 C/Keywords: heterotetramer; immunoglobulin

Query Match  
 Best Local Similarity 19.9%; Score 27; DB 2; Length 16;  
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Db 16 IKAPGKAP 25  
 7 IGSTFGARAP 16

RESULT 4  
 A41439  
 acid ribonuclease (EC 3.1.-.-) - bovine (fragment)  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 21-Apr-1992 #sequence\_revision 21-Apr-1992 #text\_change 09-Jul-2004  
 C/Accession: A41439  
 R/Ohg1, K.; Sanda, A.; Takizawa, Y.; Irie, M.  
 J. Biochem. 103, 267-273, 1988  
 A/Title: Purification of acid ribonucleases from bovine spleen.  
 A/Reference number: A41439; MUID:88227899; PMID:3131316  
 C/Accession: A41439  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <OHG>  
 A/Cross-references: UNIPROT:Q7M2NS  
 C/Keywords: hydrolase

Query Match  
 Best Local Similarity 19.9%; Score 27; DB 2; Length 20;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Db 5 HPHLPKDI 12  
 9 HLYFPKDL 16

RESULT 5  
 ZJBRG4  
 gene J protein - phage G4  
 C/Species: phage G4  
 C/Date: 30-Nov-1979 #sequence\_revision 30-Nov-1979 #text\_change 09-Jul-2004  
 C/Accession: A04259  
 R/Godson, G.N.; Barrell, B.G.; Staden, R.; Fiddes, J.C.  
 Nature 276, 236-247, 1978  
 A/Title: Nucleotide sequence of bacteriophage G4 DNA.  
 A/Reference number: A93200; MUID:79053264; PMID:714153  
 C/Accession: A04259  
 A/Molecule type: DNA  
 A/Residues: 1-25 <GOD>  
 A/Cross-references: UNIPROT:P03652; GB:J02454; GB:M10724; GB:M11404; GB:V00657; NID:g156  
 C/Comment: Gene J protein is one of the structural components of the bacteriophage coat.  
 C/Keywords: DNA binding

Query Match  
 Best Local Similarity 19.9%; Score 27; DB 1; Length 25;  
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
 Db 8 LPKDIVRSIAKPKR 23  
 : | | | | | | |

Db 1 MKKSIRSGKSKAR 16

RESULT 6  
 A36016  
 granulocyte inhibitory protein - human  
 C/Species: Homo sapiens (man)  
 C/Date: 11-Jan-1991 #sequence\_revision 11-Jan-1991 #text\_change 09-Jul-2004  
 C/Accession: A36016  
 R/Hoerl, W.H.; Haag-Weber, M.; Georgopoulos, A.; Block, L.H.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 6353-6357, 1990  
 A/Title: Physicochemical characterization of a polypeptide present in uremic serum that  
 A/Reference number: A36016; MUID:90349614; PMID:2385596  
 C/Accession: A36016  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-20 <HOB>  
 A/Cross-references: UNIPROT:Q7M4S4  
 C/Supfamily: immunoglobulin V region; immunoglobulin homology

Query Match  
 Best Local Similarity 19.5%; Score 26.5; DB 2; Length 20;  
 Matches 7; Conservative 5; Mismatches 2; Indels 5; Gaps 1;  
 Db 11 DIVR-----STAKPKRA 24  
 1 DIVMTQSPPTLVSPPGERA 19

RESULT 7  
 PQ0143  
 polygalacturonase (EC 3.2.1.15) p26 - evening primrose (fragment)  
 C/Species: Oenothera organensis (evening primrose)  
 C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
 C/Accession: PQ0143  
 R/Brown, S.M.; Crouch, M.L.  
 Plant Cell 2, 263-274, 1990  
 A/Title: Characterization of a gene family abundantly expressed in *Oenothera organensis*  
 A/Reference number: JQ0992; MUID:93005658; PMID:2152116  
 C/Accession: PQ0143  
 A/Molecule type: mRNA  
 A/Residues: 1-22 <BRO>  
 A/Cross-references: UNIPROT:Q9S9B8  
 A/Experimental source: pollen  
 C/Comment: This protein is specifically translated in the pollens.  
 Y growing tube.  
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match  
 Best Local Similarity 19.5%; Score 26.5; DB 2; Length 22;  
 Matches 8; Conservative 3; Mismatches 9; Indels 1; Gaps 1;  
 Db 1 CRVTHPLPDYRSIAKAPG 21  
 1 CTTTNAQL-FDITKYGAKDGG 20

RESULT 8  
 S32551  
 glutathione transferase (EC 2.5.1.18) mu (isoform pi 6.4) - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 02-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 09-Jul-2004  
 C/Accession: S32551; S32550  
 R/Singhal, S.S.; Saxena, M.; Ahmad, H.; Anaschi, Y.C.  
 Biochim. Biophys. Acta 1116, 137-146, 1992  
 A/Title: Glutathione S-transferases of mouse liver: sex-related differences in the expe  
 A/Reference number: S32546; MUID:92256466; PMID:1581342  
 C/Accession: S32551  
 A/Molecule type: protein  
 A/Residues: 1-13 <SINI>  
 A/Cross-references: UNIPROT:Q7M059  
 A/Experimental source: female

A/Accession: S32550  
 A/Molecule type: protein  
 A/Residues: 1-13 <SIN2>  
 A/Experimental source: male  
 C/Keywords: transferase

Query Match 19.1%; Score 26; DB 2; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RATHP 6  
 DB 9 RLTHP 13

## RESULT 9

I38336  
 hypothetical TEL/MN1 mutant fusion protein type I - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 21-Feb-1997 #sequence\_rev1sion 21-Feb-1997 #text\_change 20-Apr-2000  
 C/Accession: I38336  
 R/Buil's, A.; Sherr, S.; van Bael, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.  
 Oncogene 10, 1511-1519, 1995  
 A/Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion  
 A/Reference number: I38031; MUID:95249265; PMID:7731705  
 A/Accession: I38336  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-15 <BUI>  
 A/Cross-references: EMBL:X85026; NID:G971473; PIDN:CA59399.1; PID:G971474  
 C/Comment: This sequence is the chimeric product of a translocation mutation.  
 C/Genetic:  
 A/Gene: ETV6/MN1, TEL/MN1  
 A/Map position: 22q11/12p13  
 C/Keywords: fusion protein

Query Match 19.1%; Score 26; DB 4; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 HLPKDI 12  
 DB 6 HLPKDI 11

## RESULT 10

JP0055  
 ribosomal protein L30 - Bacillus polymyxa (fragment)  
 C/Species: Bacillus polymyxa  
 C/Date: 10-Mar-1994 #sequence\_rev1sion 28-Oct-1994 #text\_change 09-Jul-2004  
 C/Accession: JP0055  
 R/Ochi, K.  
 submitted to JIPID, February 1994  
 A/Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr  
 A/Reference number: JP0042

A/Accession: JP0055  
 A/Molecule type: protein  
 A/Residues: 1-20 <OCH>  
 A/Cross-references: UNIPROT:Q7M163  
 C/Superfamily: Escherichia coli ribosomal protein L30  
 C/Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 IYRSIAKAPG 21  
 DB 7 LVRSLSIRPG 16

## RESULT 11

H30608  
 Ig kappa chain V-III region (Ste) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence\_rev1sion 29-Jun-1989 #text\_change 09-Jul-2004  
 C/Accession: H30608  
 R/Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Sol  
 J. Immunol. 142, 3158-3163, 1989  
 A/Title: Structural and idiotypic characterization of the L chains of human IGM autocal  
 A/Reference number: A30601; MUID:89215279; PMID:2496160  
 A/Accession: H30608  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-22 <GON>  
 A/Cross-references: UNIPROT:Q9UL78  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;  
 Best Local Similarity 40.0%; Pred. No. 3e+03;  
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIAKAPKRA 24  
 DB 10 TLSVSPGERA 19

## RESULT 12

D30609  
 Ig kappa chain V-III regions (Jon and Mit) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence\_rev1sion 29-Jun-1989 #text\_change 09-Jul-2004  
 C/Accession: D30609  
 R/Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Sol  
 J. Immunol. 142, 3158-3163, 1989  
 A/Title: Structural and idiotypic characterization of the L chains of human IGM autocal  
 A/Reference number: A30601; MUID:89215279; PMID:2496160  
 A/Accession: D30609  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-22 <GON>  
 A/Cross-references: UNIPROT:Q9UL85  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;  
 Best Local Similarity 40.0%; Pred. No. 3e+03;  
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIAKAPKRA 24  
 DB 10 TLSVSPGERA 19

## RESULT 13

B30609  
 Ig kappa chain V-III region (She) - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Jun-1989 #sequence\_rev1sion 29-Jun-1989 #text\_change 09-Jul-2004  
 C/Accession: B30609  
 R/Gonl, F.R.; Chen, P.P.; McGinnis, D.; Arjona, M.L.; Fernandez, J.; Carson, D.; Sol  
 J. Immunol. 142, 3158-3163, 1989  
 A/Title: Structural and idiotypic characterization of the L chains of human IGM autocal  
 A/Reference number: A30601; MUID:89215279; PMID:2496160  
 A/Accession: B30609  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-24 <GON>  
 A/Cross-references: UNIPROT:Q9UL83  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 24;  
 Best Local Similarity 40.0%; Pred. No. 3.3e+03;  
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIKAPKRA 24  
 ::: : ||: ||  
 Db 10 TUSVSPERA 19

## RESULT 14

JP0052  
 ribosomal protein l30 - *Bacillus macquariensis* (fragment)  
 C/Species: *Bacillus macquariensis*  
 C/Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
 C/Accession: JP0052  
 R/Ochi, K.  
 submitted to JIPID, February 1994  
 A/Description: Phylogenetic diversity in the genus *Bacillus* and comparative ribosomal pr  
 A/Reference number: JP0042  
 A/Accession: JP0052  
 A/Molecule type: protein  
 A/Residues: 1-24 <OCH>  
 A/Cross-references: UNIPROT:Q7M162  
 C/Superfamily: *Bacterichia coli* ribosomal protein l30  
 C/Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 24;  
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 IVRSIAKPG 21  
 : ||: ||  
 Db 8 LVRSILGRPG 17

## RESULT 15

H37196  
 bradykinin-potentiating peptide 8 - *Island jararaca*  
 C/Species: *Bothrops insularis* (*Island jararaca*)  
 C/Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 09-Jul-2004  
 C/Accession: H37196  
 R/Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
 J. Protein Chem. 9, 221-227, 1990  
 A/Title: Primary structure and biological activity of bradykinin potentiating peptides f  
 A/Reference number: A37196; WUID:90351557; PMID:2386615  
 A/Accession: H37196  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-10 <CIN>  
 A/Cross-references: UNIPROT:P30426  
 C/Keywords: pyroglutamic acid  
 F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.4%; Score 25; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 HPNIP 9  
 ||: ||  
 Db 5 HPNIP 9

Search completed: February 22, 2005, 07:20:44  
 UOB time : 40 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2005, 07:01:55 ; Search time 175 Seconds

(without alignments)  
73.154 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136

Sequence: 1 CRVTHPHLPKDVRISAKAPGKAP 25

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 16988

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Uniprot 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 35    | 25.7        | 19     | 1     | CKAD CONGE  |
| 2          | 33    | 24.3        | 23     | 2     | Q6TMS4      |
| 3          | 31    | 22.8        | 18     | 1     | CTIC_LITCI  |
| 4          | 30    | 22.1        | 18     | 2     | Q9BQ70      |
| 5          | 30    | 22.1        | 19     | 2     | Q9ORH8      |
| 6          | 30    | 22.1        | 20     | 2     | Q99JV2      |
| 7          | 29    | 21.3        | 16     | 2     | Q9T2R0      |
| 8          | 29    | 21.3        | 18     | 1     | CTIA_LITCI  |
| 9          | 29    | 21.3        | 19     | 2     | Q16271      |
| 10         | 29    | 21.3        | 21     | 2     | Q6A1F4      |
| 11         | 29    | 21.3        | 25     | 1     | H2B1_ECHES  |
| 12         | 28    | 20.6        | 11     | 2     | Q7M374      |
| 13         | 28    | 20.6        | 22     | 2     | Q9MK47      |
| 14         | 28    | 20.6        | 24     | 2     | Q9L7N8      |
| 15         | 27    | 19.9        | 12     | 1     | PEK4_PBRAM  |
| 16         | 27    | 19.9        | 15     | 2     | Q9UEM3      |
| 17         | 27    | 19.9        | 20     | 2     | Q9UMI8      |
| 18         | 27    | 19.9        | 20     | 2     | Q7M2N5      |
| 19         | 27    | 19.9        | 21     | 2     | Q9NM05      |
| 20         | 27    | 19.9        | 22     | 2     | Q6UDH2      |
| 21         | 27    | 19.9        | 24     | 2     | Q7XAX3      |
| 22         | 27    | 19.9        | 25     | 1     | VGJ_BPQ4    |
| 23         | 27    | 19.9        | 25     | 2     | Q7RI27      |
| 24         | 27    | 19.9        | 25     | 2     | Q6QF50      |
| 25         | 26.5  | 19.5        | 19     | 1     | Q9TWR3      |
| 26         | 26.5  | 19.5        | 19     | 1     | TRP3_LEUMA  |
| 27         | 26.5  | 19.5        | 20     | 2     | Q7M454      |
| 28         | 26.5  | 19.5        | 22     | 2     | Q9S9B8      |
| 29         | 26    | 19.1        | 12     | 2     | Q7KYL7      |
| 30         | 26    | 19.1        | 13     | 1     | UP71_LITWM  |
| 31         | 26    | 19.1        | 13     | 2     | Q7M059      |

## ALIGNMENTS

| RESULT 1 | CKAD CONGE  | STANDARD   | PRT | 19 AA |
|----------|---|--|-----|-------|
| ID       | CKAD CONGE  | STANDARD   | PRT | 19 AA |
| DT       | 29-MAR-2004 (Rel. 43, Created)  |  |     |       |
| DT       | 29-MAR-2004 (Rel. 43, Last sequence update)                           |  |     |       |
| DT       | 25-OCT-2004 (Rel. 45, Last annotation update)                         |  |     |       |
| DE       | Alpha-conotoxin GID.  |  |     |       |
| OS       | Conus geographus (geography cone).                                    |  |     |       |
| OC       | Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;            |  |     |       |
| OC       | Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;        |  |     |       |
| OC       | Neogastropoda; Conidae; Conidae; Conus.                               |  |     |       |
| OX       | NCBI_TaxID=6491;  |  |     |       |
| RN       | [1]   |  |     |       |
| RP       | SEQUENCE, STRUCTURE BY NMR, SYNTHESIS, MASS SPECTROMETRY, AND         |  |     |       |
| RP       | NOTAGNESIS OF ARG-12.   |  |     |       |
| RC       | TISSUE=Venom;   |  |     |       |
| RX       | PubMed=12419800; DOI=10.1074/jbc.M210280200;                          |  |     |       |
| RA       | Nicke A., Loughnan M.L., Millard E.L., Alwood P.F., Adams D.J.,       |  |     |       |
| RA       | Daly N.L., Craik D.J., Lewis R.J.,                                    |  |     |       |
| RT       | "Isolation, structure, and activity of GID, a novel alpha 4/7-        |  |     |       |
| RT       | conotoxin with an extended N-terminal sequence.";                     |  |     |       |
| RL       | J. Biol. Chem. 278:3137-3144(2003).                                   |  |     |       |
| CC       | -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they    |  |     |       |
| CC       | bind to the nicotinic acetylcholine receptors (nAChR) and thus        |  |     |       |
| CC       | inhibit them. This peptide reversibly inhibits alpha-7, alpha-        |  |     |       |
| CC       | 3/beta-2, and alpha-4/beta-2 subunits.                                |  |     |       |
| CC       | -1- SUBCELLULAR LOCATION: Secreted.                                   |  |     |       |
| CC       | -1- TISSUE SPECIFICITY: Expressed by the venom duct.                  |  |     |       |
| CC       | -1- MASS SPECTROMETRY: MW=2184.9; RANGE=1-19; NOTE=Ref.1.             |  |     |       |
| CC       | -1- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type    |  |     |       |
| CC       | family.   |  |     |       |
| DR       | PDB; 1MTQ; NMR; -   |  |     |       |
| KW       | 3D-structure; Acetylcholine receptor inhibitor;                       |  |     |       |
| KW       | Direct protein sequencing; Gamma-carboxyglutamic acid; Hydroxylation; |  |     |       |
| KW       | Neurotoxin; Postsynaptic neurotoxin; Toxin; Vitamin K.                |  |     |       |
| FT       | DISULFID  | 5  | 11  |       |
| FT       | DISULFID  | 6  | 19  |       |
| FT       | MOD RES   | 4  | 4   |       |
| FT       | MOD RES   | 16   | 16  |       |
| FT       | MUTAGEN   | 12   | 12  |       |
| FT       | MUTAGEN   | 1  | 4   |       |
| SO       | SEQUENCE  | 19 AA; 2130 MW;                                    |     |       |
| SO       | SEQUENCE  | 0D14S8724C98F08 CRC64;                             |     |       |
| QY       | Query Match   | 25.7%; Score 35; DB 1; Length 19;                  |     |       |
| QY       | Best Local Similarity   | 62.5%; Pred. No. 6.3e+02;                          |     |       |
| QY       | Matches   | 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0; |     |       |
| DB       | 11 CRVTHPHV 18  |  |     |       |

## RESULT 2

Q6TMS4 PRELIMINARY; PRT; 23 AA.  
 ID Q6TMS4  
 AC Q6TMS4  
 DT 05-JUN-2004 (TREMBlrel. 27, Created)  
 DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 GN ORFNames=PSCL2.5.424.9;  
 OS Streptomyces clavuligerus.  
 OG Plasmid, PSCL2.  
 OC Bacteria; Actinobacteria; Actinobacterizidae; Actinomycetales;  
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.  
 OX NCBI\_TaxID=1901;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wu W., Roy K.L.;  
 RL Submitted (SFP-2003) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY392415; AAG93549.1; -.  
 KW Hypothetical protein; Plasmid.  
 SQ SEQUENCE 23 AA; 2374 MW; 6F371429BF49D3F8 CRC64;

Query Match 24.3%; Score 33; DB 2; Length 23;  
 Best Local Similarity 40.0%; Pred. No. 1.5e+03;  
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 RVTNPHLPKDIVERSI 16  
 DB 8 QVANATLPKDIAHRL 22

## RESULT 3

CTIC\_LITCI STANDARD; PRT; 18 AA.  
 ID CTIC\_LITCI  
 AC P81844;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Cytropin 1.2.4.  
 OS Litorea citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodytidae; Litorea.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA MEDLINE=99435977; PubMed=10504394;  
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,  
 RA Wallace J.C., Tyler M.J.;  
 RT "Host defence peptides from the skin glands of the Australian blue  
 RT ant bacterial peptide citropin 1.1.";  
 RL Eur. J. Biochem. 265:627-637(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Dorsal and submental skin glands.  
 KW Amphibian defense peptide; Direct protein sequencing.  
 SQ SEQUENCE 18 AA; 1814 MW; 500BF778D515ABD7 CRC64;

Query Match 22.8%; Score 31; DB 1; Length 18;  
 Best Local Similarity 33.3%; Pred. No. 2.3e+03;  
 Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 11 DIVRSIAKAPGRAP 25  
 DB 4 DITKVASVGLASP 18

## RESULT 4

Q9BQTO PRELIMINARY; PRT; 18 AA.  
 ID Q9BQTO

Q9BQTO;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21195339; PubMed=11297743; DOI=10.1016/S0014-5793(01)02318-3;  
 RA Holmann K., Ambrosch I., Eibling U., Micksche M., Berger W.;  
 RT "A small upstream open reading frame causes inhibition of human major  
 RT vault protein expression from a ubiquitous mRNA splice variant.";  
 RL FEBS Lett. 494:99-104(2001).  
 DR EMBL; AJ291367; CAC35315.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11CB828 CRC64;

Query Match 22.1%; Score 30; DB 2; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 3.3e+03;  
 Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 CRVTHPLP 9  
 DB 8 CRL--PHLP 14

## RESULT 5

Q9ORH8 PRELIMINARY; PRT; 19 AA.  
 ID Q9ORH8  
 AC Q9ORH8;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE Tat protein (Fragment).  
 GN Namestat;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96CG12.  
 RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/089922202753394745;  
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,  
 RA Ido B., Hayami M., Ichimura H., Parra H. Joseph.;  
 RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the  
 RT Republic of Congo.";  
 RL AIDS Res. Hum. Retroviruses 18:79-83(2002).  
 DR EMBL; AF127545; AAK84896.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 19 AA; 2210 MW; 2A83642B89068236 CRC64;

Query Match 22.1%; Score 30; DB 2; Length 19;  
 Best Local Similarity 53.8%; Pred. No. 3.4e+03;  
 Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 PHLPKDIVRSIAK 18  
 DB 7 PHSSDHDHNSLIPK 19

## RESULT 6

Q99JV2 PRELIMINARY; PRT; 20 AA.  
 ID Q99JV2  
 AC Q99JV2;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).



OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.; TISSUE=Mammary tumor. C3;  
 RU Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005653; AA005653.1; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 20 AA; 223 MW; F203F6A80A7A0429 CRC64;  
 Query Match 22.1%; Score 30; DB 2; Length 20;  
 Best Local Similarity 70.0%; Pred. No. 3.6e+03;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 13 VRSIAKAPGK 22  
 DB 1 VFSIAKAPGK 10  
 RESULT 7  
 Q9T2R0 PRELIMINARY; PRT; 16 AA.  
 AC Q9T2R0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome-c reductase 14 kDa subunit (EC 1.10.2.2) (Fragment).  
 OS Solanum tuberosum (Potato).  
 OC Mitochondrion.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94198758; PubMed=7764624;  
 RA Braun H.P., Krutz V., Schmitz U.K.;  
 RL Planta 193:99-106(1994).  
 DR GO:0008121; PubMed=7764624; BRC625F8B4AC8E7 CRC64;  
 SQ SEQUENCE 16 AA; 1946 MW; BRC625F8B4AC8E7 CRC64;  
 Query Match 21.3%; Score 29; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 4.1e+03;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 5 HPHLPKDI 12  
 DB 2 HOYLPEDL 9  
 RESULT 8  
 CTIA\_LITCI STANDARD; PRT; 18 AA.  
 ID CTIA\_LITCI  
 AC P81838;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Citropin 1.1.3.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodytidae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=94435977; PubMed=10504394;  
 RA Wegener K.L., Mohlitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,  
 Wallace J.C., Tyler M.J.;

RT "Host defence peptides from the skin glands of the Australian blue  
 RT mountains tree-frog Litoria citropa. Solution structure of the  
 RT antibacterial peptide citropin 1.1.";  
 RL Eur. J. Biochem. 265:627-637(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Dorsal and subventral skin glands.  
 KW Amphibian defense peptide; Direct protein sequencing.  
 SQ SEQUENCE 18 AA; 1814 MW; 500BF778D51F98D7 CRC64;  
 Query Match 21.3%; Score 29; DB 1; Length 18;  
 Best Local Similarity 26.7%; Pred. No. 4.6e+03;  
 Matches 4; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
 QY 11 DIVRSIAKAPGKAP 25  
 DB 4 DVIRKVASVIGLASP 18  
 RESULT 9  
 Q16271 PRELIMINARY; PRT; 19 AA.  
 ID Q16271;  
 AC Q16271;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Arginine vasopressin V2 receptor (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95086168; PubMed=7993996;  
 RA Holtzman E.J., Kolakowski L.F.Jr., Gelfman-Holtzman O., O'Brien D.G.,  
 RA Rasoulypour M., Gulliot A.P., Ausiello D.A.;  
 RT "Mutations in the vasopressin V2 receptor gene in two families with  
 RT nephrogenic diabetes insipidus.";  
 RL J. Am. Soc. Nephrol. 5:169-176(1994).  
 DR EMBL; S75754; AAB32753.1; -.  
 DR GO:0004872; F:receptor activity; IEA.  
 FT NON TER 19  
 SQ SEQUENCE 19 AA; 1905 MW; 181640EPD90F2788 CRC64;  
 Query Match 21.3%; Score 29; DB 2; Length 19;  
 Best Local Similarity 37.5%; Pred. No. 4.8e+03;  
 Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
 QY 5 HPHLPKDI VRSIAKAP 20  
 DB 4 HPSLPSCAMASLSAQP 19  
 RESULT 10  
 O6A1F4 PRELIMINARY; PRT; 21 AA.  
 ID O6A1F4;  
 AC O6A1F4;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Multiple sugar metabolism regulator (Fragment).  
 GN Name=amr;  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Ramachandran V., McArthur J.D., Behm C.E., Gutzelt C., Dorton M.,  
 RA Fagan P.K., Towers R.J., Currie B.J., Sripirakash K.S., Walker M.J.;  
 RT "Distribution and molecular evolution of the fibronectin binding  
 RT protein prf2 gene family in Streptococcus pyogenes isolated from the  
 RT Northern Territory of Australia.";

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ784873; CAH04963.1; -.  
 FT NON TER 21 21  
 SQ SEQUENCE 21 AA; 2332 MW; 2086BDCA45FE51A1 CRC64;

Query Match 21.3%; Score 29; DB 2; Length 21;  
 Best Local Similarity 45.5%; Pred. No. 5.4e+03;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 PHLPKDIYR1 16  
 DB 5 PHFPINNVRL 15

## RESULT 11

H2B1\_ECHES STANDARD; PRT; 25 AA.  
 AC P13281;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Histone H2B.1, sperm (Fragment).  
 OS Echinus asculentus (Sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoida; Euechinoidea; Echinacea; Echinoidea; Echinidae; Echinus.  
 OX NCBI\_TaxID=7648;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90126812; Pubmed=2298202;  
 RA Hall C.S., Thomas J.O.;  
 RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal tail of H2B interacts with linker DNA."  
 RL Eur. J. Biochem. 187:145-153 (1990).  
 CC -1- SUBUNIT: The nucleosome is an octamer containing two molecules  
 CC of H2A, H2B, H3 and H4. The octamer wraps approximately 146  
 CC bp of DNA.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: Belongs to the histone H2B family.  
 DR PIR; S07770; S07770.  
 DR InterPro; IPR000558; HISTONE\_H2B; PARTIAL.  
 DR PROSITE; PS00357; HISTONE\_H2B; PARTIAL.  
 KM Chromosomal protein; Direct protein sequencing; DNA-binding;  
 KM Multigene family; Nuclear protein; Nucleosome core.  
 FT NON TER 25 25  
 SQ SEQUENCE 25 AA; 2693 MW; 9842DD3D7A3A9EC CRC64;

Query Match 21.3%; Score 29; DB 1; Length 25;  
 Best Local Similarity 62.5%; Pred. No. 6.4e+03;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 18 KAFGRAP 25  
 DB 4 KSPTKRSP 11

## RESULT 12

Q7M374 PRELIMINARY; PRT; 11 AA.  
 AC Q7M374;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Ribosomal protein MRP-S24, mitochondrial (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RA Grack H.R.;  
 RL Submitted (JUL-1999) to the PIR data bank.  
 DR PIR; S78765; S78765.

FT NON TER 1 1  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1264 MW; 95F49156A32772CA CRC64;

Query Match 20.6%; Score 28; DB 2; Length 11;  
 Best Local Similarity 40.0%; Pred. No. 3.9e+03;  
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 HPPLPKDIYR 14  
 DB 2 HVDVPKDLTK 11

## RESULT 13

Q9MX47 PRELIMINARY; PRT; 22 AA.  
 AC Q9MX47;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE MHC class II antigen (Fragment).  
 GN Name=Oryz. DCB;  
 OS Oryza latipes (Medaka fish) (Japanese ricefish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;  
 OC Belontiiformes; Atherinichthyidae; Oryziatidae; Oryzias.  
 OX NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HNI;  
 RA Naruse K., Oka H., Kojima A., Beseho Y., Kuroda N., Matsuzaki T.,  
 RA Hori H., Shima A., Nonaka M.;  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB031216; BAA94283.1; -.  
 FT NON TER 1 1  
 FT NON TER 22 22  
 SQ SEQUENCE 22 AA; 2441 MW; E2AP1A9CD581F5FB CRC64;

Query Match 20.6%; Score 28; DB 2; Length 22;  
 Best Local Similarity 38.5%; Pred. No. 7.9e+03;  
 Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CRYTHPHPKDIY 13  
 DB 7 CRVHVSLKDP1T 19

## RESULT 14

Q9L7N8 PRELIMINARY; PRT; 24 AA.  
 AC Q9L7N8;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Bmpd (Fragment).  
 GN Name=bmpd;  
 OS Borrelia afzelii.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=29518;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IP3;  
 RX MEDLINE=20179823; Pubmed=10715014;  
 RX DOI=10.1128/7B.182.7.2037-2042.2000;  
 RA Gordacheva V.Y., Godfrey H.P., Cabelli F.C.;  
 RT "Analysis of the bmp gene family in Borrelia burgdorferi sensu lato."  
 DR EMBL; AF222435; AAF45174.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 24 AA; 2681 MW; 57F3887CD59126F9 CRC64;

Query Match 20.6%; Score 28; DB 2; Length 24;

Best Local Similarity 46.2%; Pred. No. 8.6e+03;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 12 IYNSIAPGKRA 24  
| | | | |  
| | | | |  
Db 1 IINGIIRAPYDKA 13

## RESULT 15

PPK4\_PPRAM STANDARD; PRT; 12 AA.  
ID PPK4\_PPRAM  
AC P82619;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Pyrokinnin-4 (Pea-PK-4) (YPRL-amide).  
OS Periplaneta americana (American cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;  
OC Blattellidae; Periplaneta.  
OX NCBI\_TaxID=6978;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE-Retrocerebral complex;  
RX MEDLINE=99212469; PubMed=1016736; DOI=10.1016/S0965-1748(98)00117-9;  
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
RT "Differential distribution of pyrokinnin-isoforms in cerebral and  
abdominal neurochemical organs of the American cockroach.";  
RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=20189894; PubMed=10723010;  
RA Predel R., Becker M.;  
RT "Tagma-specific distribution of FXPRlamides in the nervous system of  
the American cockroach.";  
RL J. Comp. Neurol. 419:352-363(2000).  
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
activity).  
CC -1- TISSUE SPECIFICITY: Corpora cardiaca.  
CC -1- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI; RANGE=1-12;  
CC NOTE=Ref.1.  
CC -1- SIMILARITY: Belongs to the pyrokinnin family.  
KW Annotation: Direct protein sequencing; Neuropeptide; Pyrokinnin.  
FT MOD\_RES 12  
FT MOD\_RES 12 Leucine amide.  
SQ SEQUENCE 12 AA; 1449 MW; FA7A3049F42CA1 CRC64;

Query Match 19.9%; Score 27; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 5.9e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 HLPKDI 12  
| | | | |  
| | | | |  
Db 2 HLPKDV 7

Search completed: February 22, 2005, 07:20:00  
Job time : 178 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 22, 2005, 07:01:10 / Search time 161 Seconds  
(Without alignments)  
60.056 Million cell updates/sec

Title: US-10-751-743-4

Sequence: 1 CRVTHPLPKDIVRSIAKAPKAP 25

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 768190

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: A\_Geneseq.16Dec04:\*

1: geneseqp19808:\*\n2: geneseqp19908:\*\n3: geneseqp20008:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 102   | 75.0        | 20     | AAW24102 | AAW24102 Canine im |
| 2          | 89    | 65.4        | 17     | AAV50894 | AAV50894 Antibody  |
| 3          | 89    | 65.4        | 17     | AAV50893 | AAV50893 Antibody  |
| 4          | 89    | 65.4        | 17     | ADQ76003 | ADQ76003 Peptide c |
| 5          | 89    | 65.4        | 25     | AAV79999 | AAV79999 Optimised |
| 6          | 79    | 58.1        | 20     | AAW24103 | AAW24103 Canine im |
| 7          | 72    | 52.9        | 17     | AAV50896 | AAV50896 Antibody  |
| 8          | 72    | 52.9        | 17     | ADQ76005 | ADQ76005 Peptide c |
| 9          | 69    | 50.7        | 17     | AAV50895 | AAV50895 Antibody  |
| 10         | 69    | 50.7        | 17     | ADQ76004 | ADQ76004 Peptide c |
| 11         | 68    | 50.0        | 25     | AAV80000 | AAV80000 Optimised |
| 12         | 65    | 47.8        | 17     | AAV50898 | AAV50898 Antibody  |
| 13         | 65    | 47.8        | 17     | ADQ76007 | ADQ76007 Peptide c |
| 14         | 64    | 47.1        | 25     | AAV68602 | AAV68602 Peptide s |
| 15         | 64    | 47.1        | 25     | AAV91212 | AAV91212 Modified  |
| 16         | 64    | 47.1        | 25     | AAV79998 | AAV79998 Optimised |
| 17         | 63    | 46.3        | 25     | AAV80077 | AAV80077 Optimised |
| 18         | 61    | 44.9        | 17     | AAV50897 | AAV50897 Antibody  |
| 19         | 61    | 44.9        | 17     | ADQ76006 | ADQ76006 Peptide c |
| 20         | 60    | 44.1        | 14     | AAO18028 | AAO18028 Human imm |
| 21         | 60    | 44.1        | 14     | ABU00529 | ABU00529 Human IGE |
| 22         | 60    | 44.1        | 16     | AAO18018 | AAO18018 Human imm |
| 23         | 60    | 44.1        | 16     | AAO18041 | AAO18041 Human imm |
| 24         | 60    | 44.1        | 16     | ADG17011 | ADG17011 Human imm |
| 25         | 60    | 44.1        | 16     | ADG17005 | ADG17005 Human imm |

|    |    |      |    |          |                    |
|----|----|------|----|----------|--------------------|
| 26 | 60 | 44.1 | 17 | ADG17049 | ADG17049 Disulphid |
| 27 | 60 | 44.1 | 18 | AAO18030 | AAO18030 Human imm |
| 28 | 60 | 44.1 | 18 | AAO18019 | AAO18019 Human imm |
| 29 | 60 | 44.1 | 18 | AAO18042 | AAO18042 Human imm |
| 30 | 60 | 44.1 | 18 | AAO18036 | AAO18036 Human imm |
| 31 | 60 | 44.1 | 18 | ABJ00531 | ABJ00531 Human IGE |
| 32 | 60 | 44.1 | 18 | ABJ00537 | ABJ00537 Human IGE |
| 33 | 60 | 44.1 | 18 | ADG17020 | ADG17020 Human imm |
| 34 | 60 | 44.1 | 18 | ADG17006 | ADG17006 Human imm |
| 35 | 60 | 44.1 | 18 | ADG17012 | ADG17012 Human imm |
| 36 | 60 | 44.1 | 18 | ADG17014 | ADG17014 Human imm |
| 37 | 60 | 44.1 | 20 | AAO18031 | AAO18031 Human imm |
| 38 | 60 | 44.1 | 20 | AAO18037 | AAO18037 Human imm |
| 39 | 60 | 44.1 | 20 | ABJ00532 | ABJ00532 Human IGE |
| 40 | 60 | 44.1 | 20 | ABJ00538 | ABJ00538 Human IGE |
| 41 | 60 | 44.1 | 20 | ADG17019 | ADG17019 Human imm |
| 42 | 60 | 44.1 | 20 | ADG17013 | ADG17013 Human imm |
| 43 | 60 | 44.1 | 21 | ADG17044 | ADG17044 Human imm |
| 44 | 60 | 44.1 | 21 | ADG17026 | ADG17026 Human imm |
| 45 | 60 | 44.1 | 21 | ADG17038 | ADG17038 Human imm |

# ALIGNMENTS

RESULT 1  
ID AAW24102 standard; peptide; 20 AA.  
XX AAW24102;  
AC  
XX 21-NOV-1997 (first entry)  
DT  
XX Canine Immunoglobulin E peptide 5.  
DE  
XX  
XX Immunoglobulin E; IGE; anti-canine IGE antibody; allergy; canine; dog.  
KW  
XX  
XX Canis familiaris.  
OS  
XX  
XX JF09169795-A.  
PN  
XX 30-JUN-1997.  
PD  
XX  
XX 22-DEC-1995; 95JP-00334381.  
PF  
XX 22-DEC-1995; 95JP-00334381.  
PR  
XX 22-DEC-1995; 95JP-00334381.  
XX  
PA (HITB) HITACHI CHEM CO LTD.  
XX  
XX WPI, 1997-389423/36.  
DR N-PSDB; AAT85651.  
DR  
XX Canine Immunoglobulin E peptide fragment and related DNA - useful for the preparation of anti-canine immunoglobulin E antibody.  
PT  
XX  
XX Claim 2, Page 9, 12pp; Japanese.  
PS  
XX  
XX AAW24098-106 are peptide fragments containing at least 5 continuous amino acids of the partial canine immunoglobulin E (IGE) protein shown in CC AAW24097. The peptides are used for the preparation of anti-canine IGE antibody. The anti-canine IGE antibody can be used for the diagnosis of CC canine allergies  
CC  
XX  
XX Sequence 20 AA;  
SQ  
Query Match 75.0%; Score 102; DB 2; Length 20;  
Best local similarity 100.0%; Pred. No. 1.7e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CRVTHPLPKDIVRSIAKA 19  
|||  
Db 2 CRVTHPLPKDIVRSIAKA 20

RESULT 2  
AAVS0894  
ID AAVS0894 standard; peptide; 17 AA.  
XX  
AC AAVS0894;  
XX  
DT 24-FEB-2000 (first entry)  
XX  
DE Antibody 15A.2 canine IGE binding epitope 1.  
XX  
KM Canine; allergy; antibody 15A.2; IGE; B cell; mast cell; anti-allergy;  
XX epitope; prophylaxis; treatment; mimotope.  
XX  
OS Synthetic.  
XX  
PN EP957111-A2.  
XX  
PD 17-NOV-1999.  
XX  
PF 09-APR-1999; 99EP-00107035.  
XX  
PR 09-APR-1998; 98US-00058331.  
XX 30-MAR-1999; 99US-00281760.  
XX  
PA (IDEX-) IDEXX LAB INC.  
XX  
PI Lawton R, Mermer B, Francoeur G;  
XX  
DR WPI; 2000-040833/04.  
XX  
PT Binding proteins used for treatment or prophylaxis of canine allergy.  
XX  
PS Disclosure; Fig 7; 30pp; English.  
XX  
CC This invention describes a novel binding protein which specifically binds  
CC to native canine free or B-cell bound IGE, and which doesn't bind to IGE  
CC when the IGE is bound to mast cells. The peptide products of the  
CC invention have anti-allergic activity. The antibodies bind to defined  
CC epitopes on free or B-cell bound IGE molecules which have an important  
CC role in allergic reaction. The specific binding proteins are used to  
CC produce a pharmaceutical composition, preferably with a diluent, which  
CC can be used for prophylaxis or treatment of canine allergy. AAVS0876-  
CC Y50900 represent peptide mimotopes used in the method of the invention  
SQ  
Sequence 17 AA;  
Query Match 65.4%; Score 89; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRVTHPHLPKDIVRSI 16  
DB 2 CRVTHPHLPKDIVRSI 17  
RESULT 3  
AAVS0893  
ID AAVS0893 standard; peptide; 17 AA.  
XX  
AC AAVS0893;  
XX  
DT 24-FEB-2000 (first entry)  
XX  
DE Antibody 15A.2 binding peptide 10 from PhdC7c phage display library.  
XX  
KM Canine; allergy; antibody 15A.2; IGE; B cell; mast cell; anti-allergy;  
XX epitope; prophylaxis; treatment; mimotope.  
XX  
OS Synthetic.  
XX  
PN EP957111-A2.  
XX

PD 17-NOV-1999.  
XX  
PF 09-APR-1999; 99EP-00107035.  
XX  
PR 09-APR-1998; 98US-00058331.  
XX 30-MAR-1999; 99US-00281760.  
XX  
PA (IDEX-) IDEXX LAB INC.  
XX  
PI Lawton R, Mermer B, Francoeur G;  
XX  
DR WPI; 2000-040833/04.  
XX  
PT Binding proteins used for treatment or prophylaxis of canine allergy.  
XX  
PS Disclosure; Fig 6; 30pp; English.  
XX  
CC This invention describes a novel binding protein which specifically binds  
CC to native canine free or B-cell bound IGE, and which doesn't bind to IGE  
CC when the IGE is bound to mast cells. The peptide products of the  
CC invention have anti-allergic activity. The antibodies bind to defined  
CC epitopes on free or B-cell bound IGE molecules which have an important  
CC role in allergic reaction. The specific binding proteins are used to  
CC produce a pharmaceutical composition, preferably with a diluent, which  
CC can be used for prophylaxis or treatment of canine allergy. AAVS0876-  
CC Y50900 represent peptide mimotopes used in the method of the invention  
SQ  
Sequence 17 AA;  
Query Match 65.4%; Score 89; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e-06;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRVTHPHLPKDIVRSI 16  
DB 2 CRVTHPHLPKDIVRSI 17  
RESULT 4  
ADQ76003  
ID ADQ76003 standard; peptide; 17 AA.  
XX  
AC ADQ76003;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Peptide capable of preventing IGE binding to high affinity receptor #2.  
XX  
KM allergy; allergic symptom; IGE binding.  
XX  
OS Synthetic.  
XX  
PN WO2004058799-A2.  
XX  
PD 15-JUL-2004.  
XX  
PE 19-DEC-2003; 2003WO-US040711.  
XX  
PR 20-DEC-2002; 2002US-00325375.  
XX  
PA (IDEX-) IDEXX LAB INC.  
XX  
PI Krahn ER, Lawton R;  
XX  
DR WPI; 2004-534123/51.  
XX  
PT New isolated polypeptides and encoding polynucleotides, useful for  
PT preventing and/or treating allergic diseases and allergy symptoms in  
PT mammals.  
XX  
PS Claim 5; SEQ ID NO 2; 50pp; English.  
XX  
CC The present invention relates to isolated polypeptides capable of

CC inhibiting the binding of IGB to a high affinity receptor. These are  
 CC useful for the prevention and/or treatment of allergic diseases and  
 CC allergy symptoms in mammals. The present sequence is a polypeptide of the  
 CC invention.

XX Sequence 17 AA;

Query Match 65.4%; Score 89; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.4e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRVTHPHLPKDIYRSI 16

Db 2 CRVTHPHLPKDIYRSI 17

RESULT 5

AAV79999 standard; peptide; 25 AA.

XX AAV79999;

XX 15-MAY-2000 (first entry)

DE Optimised IGE-CH3 domain antigen peptide for dog IGB.

KW Immunoglobulin E; IGB; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

OS Canis sp.  
 OS Synthetic.

XX WO967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

PT Now antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 PT for immunization against allergy.

PS Claim 1; Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IGE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IGB, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IGB synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IGB-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAV79994 to AAV80084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX Sequence 25 AA;

Query Match 65.4%; Score 89; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RVTHPHLPKDIYRSIAK 18

Db 8 RVTHPHLPKDIYRSIAK 24

RESULT 6

AAW24103 standard; peptide; 20 AA.

XX AAW24103;

XX 21-NOV-1997 (first entry)

DE Canine Immunoglobulin B peptide 6.

KW Immunoglobulin B; IGB; anti-canine IGB antibody; allergy; canine; dog.

XX Canis familiaris.

XX JP09169795-A.

XX 30-JUN-1997.

XX 22-DEC-1995; 95JP-00334381.

XX 22-DEC-1995; 95JP-00334381.

XX (HITB) HITACHI CHEM CO LTD.

XX WPI; 1997-389423/36.

XX N-PSDB; AAT85652.

PT Canine immunoglobulin B peptide fragment and related DNA - useful for the  
 PT preparation of anti-canine immunoglobulin B antibody.

XX Claim 2; Page 9; 12pp; Japanese.

XX AAW24098-106 are peptide fragments containing at least 5 continuous amino  
 CC acids of the partial canine immunoglobulin B (IGB) protein shown in  
 CC AAW24097. The peptides are used for the preparation of anti-canine IGB  
 CC antibody. The anti-canine IGB antibody can be used for the diagnosis of  
 CC canine allergies

XX Sequence 20 AA;

Query Match 58.1%; Score 79; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.1e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KDIYRSIAKAPGRAP 25

Db 1 KDIYRSIAKAPGRAP 16

RESULT 7

AAV50896 standard; peptide; 17 AA.

XX AAV50896;

XX 24-FEB-2000 (first entry)

DE Antibody 15A.2 green monkey IGB binding epitope 1.

KW Canine; allergy; antibody 15A.2; IGB; B cell; mast cell; anti-allergy;  
 KW epitope; prophylaxis; treatment; mimotope.

XX Synthetic.

```

XX The present invention relates to isolated polypeptides capable of
CC inhibiting the binding of Igs to a high affinity receptor. These are
CC useful for the prevention and/or treatment of allergic diseases and
CC allergy symptoms in mammals. The present sequence is a polypeptide of the
CC invention.
XX
SQ Sequence 17 AA;

Query Match          52.9%; Score 72; DB 8; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.0062;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0
QY      1 CRVTHPHLPKDIVRS 15
        |||||:::||
Db       2 CRVTHPHLPALVRS 16

RESULT 9
AAVS0895
ID AAVS0895 standard; peptide; 17 AA.
AC
AY50895;
AT
DT 24-FEB-2000 (first entry)
DE Antibody 15A.2 human IgB binding epitope 1.
KW Canine; allergy; antibody 15A.2; IgB; B cell; mast cell; anti-allergy;
epitope; prophylaxis; treatment; mimotope.
OS Synthetic.
PN EP957111-A2.
PD 17-NOV-1999.
PF 09-APR-1999; 99EP-00107035.
PR 09-APR-1998; 98US-00058331.
PS 30-MAR-1999; 99US-00281760.
PA (INDEX-) IDEXX LAB INC.
PI Lawton R, Mermer B, Francoeur G;
DR WPI; 2000-040833/04.
XX Binding proteins used for treatment or prophylaxis of canine allergy.
XX Disclosure; Fig 7; 30pp; English.
XX This invention describes a novel binding protein which specifically binds
XX to native canine free or B-cell bound IGE, and which doesn't bind to IGB
XX when the IGB is bound to mast cells. The peptide products of the
XX invention have anti-allergic activity. The antibodies bind to defined
XX epitopes on free or B-cell bound IGB molecules which have an important
XX role in allergic reaction. The specific binding proteins are used to
XX produce a pharmaceutical composition, preferably with a diluent, which
XX can be used for prophylaxis or treatment of canine allergy. AAVS0876-
XX Y50900 represent peptide mimotopes used in the method of the invention
XX
SQ Sequence 17 AA;

Query Match          50.7%; Score 69; DB 3; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0018;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY      1 CRVTHPHLPKDIVRS 15
        |||||:::||
Db       2 CRVTHPHLPALVRS 16

```



```

RESULT 10
ADQ76004
ID ADQ76004 standard; peptide; 17 AA.
XX
AC ADQ76004;
XX
DT 07-OCT-2004 (first entry)
XX
DE Peptide capable of preventing Igb binding to high affinity receptor #3.
XX
KM allergy; allergic symptom; Igb binding.
XX
OS Synthetic.
XX
PN WO2004058799-A2.
XX
PD 15-JUL-2004.
XX
PF 19-DEC-2003; 2003WO-US040711.
XX
PR 20-DEC-2002; 2002US-00325375.
XX
PA (INDEX-) IDEXX LAB INC.
XX
PI Krah ER, Lawton R;
XX
DR WPI, 2004-534123/51.
XX
PT New isolated polypeptides and encoding polynucleotides, useful for
PT preventing and/or treating allergic diseases and allergy symptoms in
PT mammals.
XX
PS Claim 5, SEQ ID NO 3; 50pp; English.
XX
CC The present invention relates to isolated polypeptides capable of
CC inhibiting the binding of Igb to a high affinity receptor. These are
CC useful for the prevention and/or treatment of allergic diseases and
CC allergy symptoms in mammals. The present sequence is a polypeptide of the
CC invention.
XX
SQ Sequence 17 AA;

Query Match 50.7%; Score 69; DB 8; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0018;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIYRS 15
   |||||: :||
   |||||: :||
Db 2 CRVTHPHLPRAIMRS 16

RESULT 11
AAV80000
ID AAV80000 standard; peptide; 25 AA.
XX
AC AAV80000;
XX
DT 15-MAY-2000 (first entry)
XX
DE Optimised Igb-CH3 domain antigen peptide for rat Igb.
XX
KM Immunoglobulin E; Igb; epsilon heavy chain; antigenic; antigen;
KM immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
KM antibody; allergy; allergic disease; immunisation; anti-allergic;
KM anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX
OS Rattus sp.
XX
OS Synthetic.
XX
PN WO967293-A1.
XX
PD 29-DEC-1999.
XX

```

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PF 21-JUN-1999; 99WO-US013959.
XX
PR 20-JUN-1998; 98US-00100287.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY, Walfield AM;
XX
DR WPI, 2000-160578/14.
XX
PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
PT for immunization against allergy.
XX
PS Claim 1; Page 99; 155pp; English.
XX
CC The present invention describes immunoglobulin E (Igb)-CH3 domain
CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and
CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for
CC a target effector site on the epsilon-heavy chain of Igb, and so
CC preventing triggering and activation of mast cells and basophils and
CC downregulation of Igb synthesis. Conjugates, or fusion peptides,
CC containing (I) are used for active immunisation against Igb-mediated
CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy
CC dermatitis. Nucleic acids that encode these compounds are useful for
CC recombinant production of corresponding peptides or in DNA vaccines.
CC Conjugates of (I) that include a promiscuous T helper cell epitope
CC (functional in genetically diverse subjects), in addition to a B cell
CC target epitope, have increased immunogenicity and may include cyclic
CC constraints (disulfide bridge) to stabilise conformational features and
CC maximize cross-reactivity to the natural target. They induce safe (non-
CC anaphylactogenic) antibodies. AAV79994 to AAV80084 represent amino acid
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 25 AA;

Query Match 50.0%; Score 68; DB 3; Length 25;
Best Local Similarity 76.5%; Pred. No. 0.004;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIYRSIAK 18
   |||||: :||
   |||||: :||
Db 8 RVDHPHPKPIYRSITK 24

RESULT 12
AAV50898
ID AAV50898 standard; peptide; 17 AA.
XX
AC AAV50898;
XX
DT 24-FEB-2000 (first entry)
XX
DE Antibody 15A.2 swine Igb binding epitope 1.
XX
KM Canine; allergy; antibody 15A.2; Igb; B cell; mast cell; anti-allergy;
KM epitope; prophylaxis; treatment; minotome.
XX
OS Synthetic.
XX
PN EP957111-A2.
XX
PD 17-NOV-1999.
XX
PR 09-APR-1999; 99EP-00107035.
XX
PR 09-APR-1998; 98US-00058331.
XX
PR 30-MAR-1999; 99US-00281760.
XX
PA (INDEX-) IDEXX LAB INC.
XX
PI Lawton R, Mermer B, Francoeur G;
XX
DR WPI, 2000-040833/04.
XX

```

XX Binding proteins used for treatment or prophylaxis of canine allergy.  
 PT  
 XX  
 PS Disclosure; Fig 7; 30pp; English.

CC This invention describes a novel binding protein which specifically binds  
 CC to native canine free or B-cell bound IGE, and which doesn't bind to IGE  
 CC when the IGE is bound to mast cells. The peptide products of the  
 CC invention have anti-allergic activity. The antibodies bind to defined  
 CC epitopes on free or B-cell bound IGE molecules which have an important  
 CC role in allergic reaction. The specific binding proteins are used to  
 CC produce a pharmaceutical composition, preferably with a diluent, which  
 CC can be used for prophylaxis or treatment of canine allergy. AAY50876-  
 CC Y50900 represent peptide mimotopes used in the method of the invention  
 XX  
 SQ Sequence 17 AA;

Query Match 47.8%; Score 65; DB 3; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 0.0075;  
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSI 16  
 DB 2 CAVTHPDLKPKIRSI 17

## RESULT 13

ID ADQ76007 standard; peptide; 17 AA.

AC ADQ76007;

DT 07-OCT-2004 (first entry)

DE Peptide capable of preventing IGE binding to high affinity receptor #6.

KW allergy; allergic symptom; IGE binding.

OS Synthetic.

PN WO2004058799-A2.

PD 15-JUL-2004.

PF 19-DEC-2003; 2003WO-US040711.

PR 20-DEC-2002; 2002US-00325375.

PA (INDEX-) IDEXX LAB INC.

PI Krah ER, Lawton R;

DR WPI; 2004-534123/51.

PT New isolated polypeptides and encoding polynucleotides, useful for  
 PT preventing and/or treating allergic diseases and allergy symptoms in  
 PT mammals.

PS Claim 5; SEQ ID NO 6; 50pp; English.

CC The present invention relates to isolated polypeptides capable of  
 CC inhibiting the binding of IGE to a high affinity receptor. These are  
 CC useful for the prevention and/or treatment of allergic diseases and  
 CC allergy symptoms in mammals. The present sequence is a polypeptide of the  
 CC invention.  
 XX  
 SQ Sequence 17 AA;

Query Match 47.8%; Score 65; DB 8; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 0.0075;  
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSI 16

DB 2 CAVTHPDLKPKIRSI 17

## RESULT 14

ID AAY68602 standard; peptide; 25 AA.

AC AAY68602;

DT 05-MAY-2000 (first entry)

DE Peptide sequence of the invention.

KW Helper T cell epitope; peptide immunogen; LHRH;  
 KW luteinizing hormone-releasing hormone; spermatogenesis; ovulation;  
 KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;  
 KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;  
 KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.  
 XX

OS Unidentified.

PN WO966952-A1.

PD 29-DEC-1999.

PF 21-JUN-1999; 99WO-US013960.

PR 20-JUN-1998; 98US-00100414.

PA (UNBI-) UNITED BIOMEDICAL INC.

PI Wang CY;

DR WPI; 2000-160562/14.

PT New peptide immunogen containing luteinizing hormone-releasing hormone  
 PT antigen site and helper T cell epitope, for e.g. contraception and  
 PT treatment of cancer.

PS Disclosure; Page 92; 102pp; English.

CC The specification describes peptide immunogens comprising a synthetic  
 CC helper T cell (Th) epitope and a target antigen, luteinizing hormone-  
 CC releasing hormone (LHRH). The peptide immunogens cause induction of a  
 CC specific immune response to LHRH which is involved in regulation of  
 CC spermatogenesis, ovulation, oestrus, sexual development and secretion of  
 CC sex hormones. Provision of a promiscuous T helper epitope (which is  
 CC functional in genetically diverse subjects) provides optimum  
 CC immunogenicity to the B cell epitopes of the target antigen and thus high  
 CC antibody titres against the target antigen. The peptide immunogens of the  
 CC invention are used to vaccinate against mammalian LHRH, for use as  
 CC (reversible) contraceptive; control of hormone-dependent tumours (cancer  
 CC of prostate or breast, also endometriosis); to prevent boar taint (and  
 CC improve meat quality) and for immunocastration. The present sequence  
 CC appears in the specification  
 XX

SQ Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;  
 Best Local Similarity 64.7%; Pred. No. 0.017;  
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTNPHLPKDIVRSI 18  
 DB 8 RVTNPHLPALMRSTTK 24

## RESULT 15

ID AAY91212 standard; peptide; 25 AA.

AC AAY91212;

XX 22-MAY-2000 (first entry)  
 XX Modified human Igs CH3 domain, SEQ ID NO:92.  
 DE Promiscuous T-cell epitope; measles virus F protein; MVF;  
 XX hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;  
 KM interleukin hormone releasing hormone; LHRH; contraceptive; anticancer;  
 KM somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;  
 KM foot and mouth disease virus; immunoglobulin B; IgB; anti-allergic;  
 KM Plasmodium falciparum; circumsporozoite; antimalarial; CERP;  
 KM cholesterol ester transport protein; anti-arteriosclerotic.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO966957-A2.  
 PN 29-DEC-1999.  
 PD 21-JUN-1999; 99WO-US013975.  
 XX 20-JUN-1998; 98US-00100412.  
 PR (UNBI-) UNITED BIOMEDICAL INC.  
 XX  
 XX Wang CY;  
 PI WPI; 2000-160564/14.  
 DR  
 XX  
 PT New artificial T helper cell epitope and derived immunogens with target  
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis  
 PT or human immune deficiency virus.  
 PS Example 6; Page 40; 129pp; English.  
 XX  
 CC The invention relates to novel promiscuous T helper cell epitopes (Th),  
 CC and immunogenic peptides comprising the Th epitopes of the invention  
 CC along with B cell epitopes. The Th epitopes and peptide immunogens  
 CC containing them, are used to induce a T helper cell response,  
 CC specifically against Plasmodium falciparum, cholesterol ester transport  
 CC protein (CERP) or HIV epitopes, but more generally against any pathogen,  
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and  
 CC peptide immunogens may be used for prevention and/or treatment of  
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer  
 CC immunotherapy; for inhibition of the action of interleukin hormone  
 CC releasing hormone (LHRH) for contraception, treatment of hormone-  
 CC dependent cancer, prevention of boar taint in meat, and immunocastration)  
 CC / for promoting the growth of animals; or for treating allergies or  
 CC arteriosclerosis. Incorporation of a promiscuous Th (functional in  
 CC genetically diverse subjects) into an immunogen improves capacity to  
 CC induce a strong T helper cell-mediated immune response, resulting in  
 CC production of antibodies against a target antigen. Th can replace carrier  
 CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121  
 CC represents a promiscuous T helper epitope from the measles virus F (MVF)  
 CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246  
 CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence  
 CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)  
 CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes  
 CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-  
 CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a  
 CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide  
 CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and  
 CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th  
 CC epitope. Somatostatin immunogens may be used to promote growth in  
 CC livestock. AAY91208 is a human CD4-CDR2-like domain antigenic site, and  
 CC AAY91209-Y90211 are MVF Th epitope/CD4 CDR2 antigenic peptides which may  
 CC be used to prevent HIV infection of T cells. AAY90212 is a modified  
 CC version of a human Igs (immunoglobulin B) CH3 domain, and AAY90213-Y90219  
 CC are Th epitope/Igs CH3 antigenic peptides which may be used in the  
 CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth  
 CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this  
 CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum

CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS  
 CC antigen and an MVF Th epitope and may be used in a malaria vaccine.  
 CC AAY91228-Y91231 represent CERP-derived peptides and AAY91232-Y91241 are  
 CC immunogens comprising a CERP peptide and a Th epitope which may be used  
 CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247  
 CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-  
 CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVF Th and  
 CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1  
 CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory  
 CC lysis protein epitope from Yersinia species, and hinge spacer peptide,  
 CC both of which may optionally be used in the antigenic peptides of the  
 CC invention  
 XX

SO Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;  
 Best local Similarity 64.7%; Pred. No. 0.017;  
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RTVPHLPKDIYSIAK 18  
 |||||:|:|  
 Db 8 RTVPHLPKALMRSTTK 24

Search completed: February 22, 2005, 07:16:58  
 Job time : 163 secs

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## OM protein - protein search, using sw model

Run on: February 22, 2005, 07:20:07 ; Search time 128 Seconds

(Without alignments)  
63.914 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136  
Sequence: 1 CRVTHPHLPKDVRISAKAPGRAP 25Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 298948

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                | Description         |
|------------|-------|-------------|--------|-------------------|---------------------|
| 1          | 136   | 100.0       | 25     | US-09-938-700-4   | Sequence 4, Appl1   |
| 2          | 89    | 65.4        | 17     | US-10-325-375A-2  | Sequence 2, Appl1   |
| 3          | 72    | 52.9        | 17     | US-10-325-375A-4  | Sequence 4, Appl1   |
| 4          | 69    | 50.7        | 17     | US-10-325-375A-3  | Sequence 3, Appl1   |
| 5          | 65    | 47.8        | 17     | US-10-325-375A-6  | Sequence 6, Appl1   |
| 6          | 64    | 47.1        | 23     | US-10-630-070-96  | Sequence 96, Appl1  |
| 7          | 64    | 47.1        | 23     | US-10-630-074-96  | Sequence 96, Appl1  |
| 8          | 64    | 44.3        | 17     | US-10-325-375A-5  | Sequence 5, Appl1   |
| 9          | 60    | 44.1        | 14     | US-10-304-443-107 | Sequence 107, Appl1 |
| 10         | 60    | 44.1        | 14     | US-10-362-527-313 | Sequence 313, Appl1 |
| 11         | 60    | 44.1        | 14     | US-10-415-389-20  | Sequence 20, Appl1  |
| 12         | 60    | 44.1        | 16     | US-10-304-443-97  | Sequence 97, Appl1  |
| 13         | 60    | 44.1        | 16     | US-10-304-443-120 | Sequence 120, Appl1 |

|  | 14 | 60 | 44.1 | 16 | 16 | US-10-415-389-10  | Sequence 10, Appl1  |
|--|----|----|------|----|----|-------------------|---------------------|
|  | 15 | 60 | 44.1 | 16 | 16 | US-10-415-389-33  | Sequence 33, Appl1  |
|  | 16 | 60 | 44.1 | 18 | 14 | US-10-304-443-98  | Sequence 98, Appl1  |
|  | 17 | 60 | 44.1 | 18 | 14 | US-10-304-443-109 | Sequence 109, Appl1 |
|  | 18 | 60 | 44.1 | 18 | 14 | US-10-304-443-115 | Sequence 115, Appl1 |
|  | 19 | 60 | 44.1 | 18 | 14 | US-10-304-443-121 | Sequence 121, Appl1 |
|  | 20 | 60 | 44.1 | 18 | 15 | US-10-362-527-315 | Sequence 315, Appl1 |
|  | 21 | 60 | 44.1 | 18 | 15 | US-10-362-527-321 | Sequence 321, Appl1 |
|  | 22 | 60 | 44.1 | 18 | 16 | US-10-415-389-11  | Sequence 11, Appl1  |
|  | 23 | 60 | 44.1 | 18 | 16 | US-10-415-389-22  | Sequence 22, Appl1  |
|  | 24 | 60 | 44.1 | 18 | 16 | US-10-415-389-28  | Sequence 28, Appl1  |
|  | 25 | 60 | 44.1 | 18 | 16 | US-10-415-389-34  | Sequence 34, Appl1  |
|  | 26 | 60 | 44.1 | 20 | 14 | US-10-304-443-110 | Sequence 110, Appl1 |
|  | 27 | 60 | 44.1 | 20 | 14 | US-10-304-443-116 | Sequence 116, Appl1 |
|  | 28 | 60 | 44.1 | 20 | 15 | US-10-362-527-316 | Sequence 316, Appl1 |
|  | 29 | 60 | 44.1 | 20 | 15 | US-10-362-527-322 | Sequence 322, Appl1 |
|  | 30 | 60 | 44.1 | 20 | 16 | US-10-415-389-23  | Sequence 23, Appl1  |
|  | 31 | 60 | 44.1 | 20 | 16 | US-10-415-389-29  | Sequence 29, Appl1  |
|  | 32 | 60 | 44.1 | 25 | 9  | US-09-974-449-33  | Sequence 33, Appl1  |
|  | 33 | 56 | 41.2 | 14 | 14 | US-10-304-443-96  | Sequence 96, Appl1  |
|  | 34 | 56 | 41.2 | 14 | 14 | US-10-304-443-119 | Sequence 119, Appl1 |
|  | 35 | 56 | 41.2 | 14 | 16 | US-10-415-389-9   | Sequence 9, Appl1   |
|  | 36 | 56 | 41.2 | 14 | 16 | US-10-415-389-32  | Sequence 32, Appl1  |
|  | 37 | 56 | 41.2 | 16 | 14 | US-10-304-443-108 | Sequence 108, Appl1 |
|  | 38 | 56 | 41.2 | 16 | 14 | US-10-304-443-114 | Sequence 114, Appl1 |
|  | 39 | 56 | 41.2 | 16 | 15 | US-10-362-527-314 | Sequence 314, Appl1 |
|  | 40 | 56 | 41.2 | 16 | 15 | US-10-362-527-320 | Sequence 320, Appl1 |
|  | 41 | 56 | 41.2 | 16 | 16 | US-10-415-389-21  | Sequence 21, Appl1  |
|  | 42 | 56 | 41.2 | 16 | 16 | US-10-415-389-27  | Sequence 27, Appl1  |
|  | 43 | 55 | 40.4 | 19 | 14 | US-10-322-210-3   | Sequence 3, Appl1   |
|  | 44 | 55 | 40.4 | 19 | 14 | US-10-304-443-3   | Sequence 3, Appl1   |
|  | 45 | 55 | 40.4 | 19 | 15 | US-10-362-527-62  | Sequence 62, Appl1  |

## ALIGNMENTS

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RESULT 1
US-09-938-700-4
; Sequence 4, Application US/09938700
; Patent No. US2002064525A1
; GENERAL INFORMATION:
; APPLICANT: Morsey, et al.
; TITLE OF INVENTION: Anti-1gE Vaccines
; FILE REFERENCE: P010761A
; CURRENT APPLICATION NUMBER: US/09/938, 700
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 25
; TYPE: PRT
; ORGANISM: DOG CH3/CH4 PEPTIDE SEQUENCE
US-09-938-700-4

Query Match      100.0%; Score 136; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4, 6e-12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CRVTHPHLPKDVRISAKAPGRAP 25
Db 1 CRVTHPHLPKDVRISAKAPGRAP 25

RESULT 2
US-10-325-375A-2
; Sequence 2, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krahn, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of 1gE to a High
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|                       |       |                   |       |                   |
|-----------------------|-------|-------------------|-------|-------------------|
| Query Match           | 47.1% | Score 64          | DB 17 | Length 23         |
| Best Local Similarity | 64.7% | Pred. No. 0.056   |       |                   |
| Matches               | 11    | Conservative      | 3     | Indels 0, Gaps 0, |
|                       | 2     | RVTNPHLPKDIVRSIAK | 18    |                   |

Db 7 RVTHPHLPALMRSTTK 23

RESULT 7  
US-10-630-074-96  
; Sequence 96, Application US/10630074  
; Publication No. US20050025782A1  
; GENERAL INFORMATION:  
; APPLICANT: Milich, David R.  
; APPLICANT: Billaud, Jean-Noel  
; TITLE OF INVENTION: Human Hepatitis B Virus Core Proteins as Vaccine Platforms and  
; TITLE OF INVENTION: Methods of Use Thereof  
; FILE REFERENCE: VACCINE-07971  
; CURRENT APPLICATION NUMBER: US/10/630,074  
; CURRENT FILING DATE: 2003-07-30  
; NUMBER OF SEQ ID NOS: 101  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 96  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-630-074-96

Query Match 47.1%; Score 64; DB 17; Length 23;  
Best Local Similarity 64.7%; Pred. No. 0.056;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18  
Db 7 RVTHPHLPALMRSTTK 23

RESULT 8  
US-10-325-375A-5  
; Sequence 5, Application US/10325375A  
; Publication No. US20030229021A1  
; GENERAL INFORMATION:  
; APPLICANT: IDEXX Laboratories, Inc.  
; APPLICANT: Krah, Eugene R.  
; APPLICANT: Lawton, Robert  
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of Ige to a High  
; TITLE OF INVENTION: Affinity Receptor  
; FILE REFERENCE: MBHB-01-672-B  
; CURRENT APPLICATION NUMBER: US/10/325,375A  
; CURRENT FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 5  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Isolated polypeptide that binds to Igs.  
US-10-325-375A-5

Query Match 44.9%; Score 61; DB 15; Length 17;  
Best Local Similarity 75.0%; Pred. No. 0.11;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRSI 16  
Db 2 CKVTHPDLPLVIVRSI 17

RESULT 9  
US-10-304-443-107  
; Sequence 107, Application US/10304443  
; Publication No. US20030170229A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Biologicals s.a.

APPLICANT: Peptide Therapeutics Ltd.  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45173CIP  
; CURRENT APPLICATION NUMBER: US/10/304,443  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US/09/698,906A  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatcsBQ for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Human peptide sequence  
US-10-304-443-107

Query Match 44.1%; Score 60; DB 14; Length 14;  
Best Local Similarity 69.2%; Pred. No. 0.12;  
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIV 13  
Db 1 CRVTHPHLPALM 13

RESULT 10  
US-10-362-527-313  
; Sequence 313, Application US/10362527  
; Publication No. US20040030106A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Mason, Sean  
; APPLICANT: Turnell, William Gordon  
; APPLICANT: Vinals Y De Basols, Carlota  
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
; FILE REFERENCE: B45236  
; CURRENT APPLICATION NUMBER: US/10/362,527  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/09576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: GB 0020717.5  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: PatcsBQ for Windows Version 4.0  
; SEQ ID NO 313  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial variant of Homo sapiens Igs peptide  
US-10-362-527-313

Query Match 44.1%; Score 60; DB 15; Length 14;  
Best Local Similarity 69.2%; Pred. No. 0.12;  
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIV 13  
Db 1 CRVTHPHLPALM 13

RESULT 11  
US-10-415-389-20  
; Sequence 20, Application US/10415389  
; Publication No. US20040115220A1  
; GENERAL INFORMATION:  
; APPLICANT: De Basols, Carlota Vinals Y  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45251  
; CURRENT APPLICATION NUMBER: US/10/415,389  
; CURRENT FILING DATE: 2003-04-25  
; PRIOR APPLICATION NUMBER: PCT/EP01/12932  
; PRIOR FILING DATE: 2001-10-24

```
/ PRIOR APPLICATION NUMBER: GB 0026334.3
/ PRIOR FILING DATE: 2000-10-27
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Human IGE peptide mimotope
US-10-415-389-20
```

```
Query Match          44.1%; Score 60; DB 16; Length 14;
Best Local Similarity 69.2%; Pred. No. 0.12;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 CRVTHPLPKDIYVS 13
Db 1 CRVTHPLPKALM 13
```

```
RESULT 12
US-10-304-443-97
/ Sequence 97, Application US/10304443
/ Publication No. US20030170229A1
/ GENERAL INFORMATION:
/ APPLICANT: SmithKline Beecham Biologicals s.a.
/ APPLICANT: Peptide Therapeutics Ltd.
/ TITLE OF INVENTION: Vaccine
/ FILE REFERENCE: B45173C1P
/ CURRENT APPLICATION NUMBER: US/10/304,443
/ CURRENT FILING DATE: 2002-11-26
/ PRIOR APPLICATION NUMBER: US/09/698,906A
/ PRIOR FILING DATE: 2001-02-20
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 97
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Human peptide sequence
/ FEATURE:
/ NAME/KEY: Unsure
/ LOCATION: (2)
/ OTHER INFORMATION: Where Xaa represents any 1 of 20 naturally occurring amino acids
US-10-304-443-97
```

```
Query Match          44.1%; Score 60; DB 14; Length 16;
Best Local Similarity 71.4%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 RVTTHPLPKDIYVS 15
Db 3 RVTTHPLPKALMRS 16
```

```
RESULT 13
US-10-304-443-120
/ Sequence 120, Application US/10304443
/ Publication No. US20030170229A1
/ GENERAL INFORMATION:
/ APPLICANT: SmithKline Beecham Biologicals s.a.
/ APPLICANT: Peptide Therapeutics Ltd.
/ TITLE OF INVENTION: Vaccine
/ FILE REFERENCE: B45173C1P
/ CURRENT APPLICATION NUMBER: US/10/304,443
/ CURRENT FILING DATE: 2002-11-26
/ PRIOR APPLICATION NUMBER: US/09/698,906A
/ PRIOR FILING DATE: 2001-02-20
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 120
/ LENGTH: 16
/ TYPE: PRT
```

```
/ ORGANISM: Human peptide sequence
US-10-304-443-120
```

```
Query Match          44.1%; Score 60; DB 14; Length 16;
Best Local Similarity 71.4%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 RVTTHPLPKDIYVS 15
Db 3 RVTTHPLPKALMRS 16
```

```
RESULT 14
US-10-415-389-10
/ Sequence 10, Application US/10415389
/ Publication No. US20040115220A1
/ GENERAL INFORMATION:
/ APPLICANT: De Bascols, Carlotia Vinals Y
/ TITLE OF INVENTION: Vaccine
/ FILE REFERENCE: B45251
/ CURRENT APPLICATION NUMBER: US/10/415,389
/ CURRENT FILING DATE: 2003-04-25
/ PRIOR APPLICATION NUMBER: PCT/EP01/12932
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: GB 0026334.3
/ PRIOR FILING DATE: 2000-10-27
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Human IGE peptide mimotope
/ NAME/KEY: VARIANT
/ LOCATION: (1)...(16)
/ OTHER INFORMATION: Xaa = Any Amino Acid
US-10-415-389-10
```

```
Query Match          44.1%; Score 60; DB 16; Length 16;
Best Local Similarity 71.4%; Pred. No. 0.14;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 RVTTHPLPKDIYVS 15
Db 3 RVTTHPLPKALMRS 16
```

```
RESULT 15
US-10-415-389-33
/ Sequence 33, Application US/10415389
/ Publication No. US20040115220A1
/ GENERAL INFORMATION:
/ APPLICANT: De Bascols, Carlotia Vinals Y
/ TITLE OF INVENTION: Vaccine
/ FILE REFERENCE: B45251
/ CURRENT APPLICATION NUMBER: US/10/415,389
/ CURRENT FILING DATE: 2003-04-25
/ PRIOR APPLICATION NUMBER: PCT/EP01/12932
/ PRIOR FILING DATE: 2001-10-24
/ PRIOR APPLICATION NUMBER: GB 0026334.3
/ PRIOR FILING DATE: 2000-10-27
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Human IGE peptide mimotope
US-10-415-389-33
```



Query Match 44.1%; Score 60; DB 16; Length 16;  
Best Local Similarity 71.4%; Pred. No. 0.14;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15  
| | | | | : : : |  
Db 3 RVTHPHLPRALMRS 16

Search completed: February 22, 2005, 07:32:24  
Job time : 128 secs

inis Page Blank (uspto)

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 22, 2005, 07:14:16 ; Search time 44 Seconds  
(Without alignments)  
42.414 Million cell updates/sec

Title: US-10-751-743-4

Perfect score: 136  
Sequence: 1 CRVTHPLRPDIYRSIAKGRKAP 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 218077

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCFUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 89    | 65.4        | 17     | 4     | US-09-281-760B-26 |
| 2          | 89    | 65.4        | 25     | 4     | US-09-701-623C-6  |
| 3          | 72    | 52.9        | 17     | 4     | US-09-281-760B-28 |
| 4          | 69    | 50.7        | 17     | 4     | US-09-281-760B-27 |
| 5          | 68    | 50.0        | 25     | 4     | US-09-701-623C-7  |
| 6          | 65    | 47.8        | 17     | 4     | US-09-281-760B-30 |
| 7          | 64    | 47.1        | 25     | 3     | US-09-100-414B-95 |
| 8          | 64    | 47.1        | 25     | 3     | US-09-303-323-95  |
| 9          | 64    | 47.1        | 25     | 4     | US-09-770-014-95  |
| 10         | 64    | 47.1        | 25     | 4     | US-09-701-588C-92 |
| 11         | 64    | 47.1        | 25     | 4     | US-09-701-623C-5  |
| 12         | 63    | 46.3        | 25     | 4     | US-09-701-623C-84 |
| 13         | 61    | 44.9        | 17     | 4     | US-09-281-760B-29 |
| 14         | 60    | 44.1        | 22     | 2     | US-08-232-539D-19 |
| 15         | 60    | 44.1        | 22     | 2     | US-08-232-539D-20 |
| 16         | 46    | 33.8        | 25     | 4     | US-09-701-623C-55 |
| 17         | 42    | 30.9        | 16     | 4     | US-09-281-760B-32 |
| 18         | 41    | 30.1        | 15     | 4     | US-09-701-623C-8  |
| 19         | 40    | 29.4        | 15     | 4     | US-09-281-760B-31 |
| 20         | 39    | 28.7        | 9      | 4     | US-09-281-760B-18 |
| 21         | 39    | 28.7        | 9      | 4     | US-09-281-760B-25 |
| 22         | 39    | 28.7        | 14     | 4     | US-09-281-760B-10 |
| 23         | 36    | 26.5        | 18     | 2     | US-09-017-205-52  |
| 24         | 36    | 26.5        | 22     | 2     | US-08-455-079-18  |
| 25         | 36    | 26.5        | 22     | 2     | US-08-455-079-14  |
| 26         | 35.5  | 26.1        | 22     | 1     | US-07-988-925-12  |
| 27         | 35.5  | 26.1        | 22     | 2     | US-08-362-780-12  |

|    |      |      |    |   |                    |                   |
|----|------|------|----|---|--------------------|-------------------|
| 28 | 35.5 | 26.1 | 22 | 4 | US-09-563-222C-105 | Sequence 105, App |
| 29 | 35.5 | 26.1 | 22 | 4 | US-08-478-684G-12  | Sequence 12, App1 |
| 30 | 35   | 25.7 | 22 | 3 | US-09-046-985-4    | Sequence 4, App1  |
| 31 | 35   | 25.7 | 22 | 3 | US-09-474-743-4    | Sequence 4, App1  |
| 32 | 35   | 25.7 | 22 | 3 | US-08-851-843A-208 | Sequence 208, App |
| 33 | 35   | 25.7 | 23 | 3 | US-08-974-549A-327 | Sequence 327, App |
| 34 | 35   | 25.7 | 23 | 3 | US-08-854-050-327  | Sequence 208, App |
| 35 | 35   | 25.7 | 23 | 3 | US-09-430-323-208  | Sequence 208, App |
| 36 | 35   | 25.7 | 23 | 4 | US-09-402-181B-327 | Sequence 327, App |
| 37 | 35   | 25.7 | 23 | 4 | US-09-721-456-327  | Sequence 327, App |
| 38 | 34   | 25.0 | 12 | 2 | US-08-323-686-15   | Sequence 15, App1 |
| 39 | 34   | 25.0 | 21 | 2 | US-08-480-190-80   | Sequence 80, App1 |
| 40 | 34   | 25.0 | 21 | 2 | US-08-488-379-80   | Sequence 80, App1 |
| 41 | 34   | 25.0 | 21 | 4 | US-08-475-399A-80  | Sequence 80, App1 |
| 42 | 34   | 25.0 | 21 | 4 | US-08-077-255A-80  | Sequence 80, App1 |
| 43 | 34   | 25.0 | 21 | 5 | PCT-US93-07545-80  | Sequence 80, App1 |
| 44 | 33.5 | 24.6 | 20 | 4 | US-08-861-153A-5   | Sequence 5, App1  |
| 45 | 33   | 24.3 | 18 | 4 | US-09-493-795B-79  | Sequence 79, App1 |

## ALIGNMENTS

```

RESULT 1
US-09-281-760B-26
; Sequence 26, Application US/09281760B
; Patent No. 6734287
; GENERAL INFORMATION:
; APPLICANT: Lawton, Robert
; APPLICANT: Marmer, Brian
; TITLE OF INVENTION: Specific Binding Protein for Treating
; TITLE OF INVENTION: Canine Allergy
; FILE REFERENCE: 01-1275A
; CURRENT APPLICATION NUMBER: US/09/281,760B
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 09/058,331
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatsSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-281-760B-26

Query Match      65.4% Score 89; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 CRVTHPLRPDIYRSI 16
      |||||
Db      2 CRVTHPLRPDIYRSI 17

RESULT 2
US-09-701-623C-6
; Sequence 6, Application US/09701623C
; Patent No. 6811782
; GENERAL INFORMATION:
; APPLICANT: Wang P.D., Chang Y1
; TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
; TITLE OF INVENTION: ALLERGY
; FILE REFERENCE: 1151153US1
; CURRENT APPLICATION NUMBER: US/09/701,623C
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/13959
; PRIOR FILING DATE: 1998-06-21
; PRIOR APPLICATION NUMBER: 09/100,287
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

```

/ LENGTH: 25  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-701-623C-6

Query Match 65.4%; Score 89; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 3.4e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18  
Db 8 RVTHPHLPKDIVRSIAK 24

RESULT 3  
US-09-281-760E-28  
/ Sequence 28, Application US/09281760E  
/ Patent No. 6734287  
/ GENERAL INFORMATION:  
/ APPLICANT: Lawton, Robert  
/ APPLICANT: Mermet, Brion  
/ APPLICANT: Francoeur, Greg  
/ TITLE OF INVENTION: Specific Binding Protein for Treating  
/ FILE REFERENCE: 01-1275A  
/ CURRENT APPLICATION NUMBER: US/09/281,760E  
/ PRIOR FILING DATE: 1999-03-30  
/ PRIOR APPLICATION NUMBER: 09/058,331  
/ PRIOR FILING DATE: 1998-04-09  
/ NUMBER OF SEQ ID NOS: 39  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 28  
/ LENGTH: 17  
/ TYPE: PRT  
/ ORGANISM: Cercopithecus aethiops  
US-09-281-760E-28

Query Match 52.9%; Score 72; DB 4; Length 17;  
Best Local Similarity 80.0%; Pred. No. 0.0001;  
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIVRS 15  
Db 2 CRVTHPHLPALVRS 16

RESULT 4  
US-09-281-760E-27  
/ Sequence 27, Application US/09281760E  
/ Patent No. 6734287  
/ GENERAL INFORMATION:  
/ APPLICANT: Lawton, Robert  
/ APPLICANT: Mermet, Brion  
/ APPLICANT: Francoeur, Greg  
/ TITLE OF INVENTION: Specific Binding Protein for Treating  
/ FILE REFERENCE: 01-1275A  
/ CURRENT APPLICATION NUMBER: US/09/281,760E  
/ PRIOR FILING DATE: 1999-03-30  
/ PRIOR APPLICATION NUMBER: 09/058,331  
/ PRIOR FILING DATE: 1998-04-09  
/ NUMBER OF SEQ ID NOS: 39  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 27  
/ LENGTH: 17  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-281-760E-27

Query Match 50.7%; Score 69; DB 4; Length 17;  
Best Local Similarity 73.3%; Pred. No. 0.00029;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIVRS 15  
Db 2 CRVTHPHLPALVRS 16

RESULT 5  
US-09-701-623C-7  
/ Sequence 7, Application US/09701623C  
/ Patent No. 6811782  
/ GENERAL INFORMATION:  
/ APPLICANT: Mang Ph.D., Chang Yi  
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF  
/ FILE REFERENCE: 11514153051  
/ CURRENT APPLICATION NUMBER: US/09/701,623C  
/ CURRENT FILING DATE: 2000-12-01  
/ PRIOR APPLICATION NUMBER: PCT/US99/13959  
/ PRIOR FILING DATE: 1999-06-21  
/ PRIOR APPLICATION NUMBER: 09/100,287  
/ PRIOR FILING DATE: 1998-06-20  
/ NUMBER OF SEQ ID NOS: 91  
/ SOFTWARE: Patentin Ver. 2.1  
/ SEQ ID NO 7  
/ LENGTH: 25  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-701-623C-7

Query Match 50.0%; Score 68; DB 4; Length 25;  
Best Local Similarity 76.5%; Pred. No. 0.0006;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 RVTHPHLPDIVRSIAK 18  
Db 8 RVDHPHFKDIVRSITK 24

RESULT 6  
US-09-281-760E-30  
/ Sequence 30, Application US/09281760E  
/ Patent No. 6734287  
/ GENERAL INFORMATION:  
/ APPLICANT: Lawton, Robert  
/ APPLICANT: Mermet, Brion  
/ APPLICANT: Francoeur, Greg  
/ TITLE OF INVENTION: Specific Binding Protein for Treating  
/ FILE REFERENCE: 01-1275A  
/ CURRENT APPLICATION NUMBER: US/09/281,760E  
/ CURRENT FILING DATE: 1999-03-30  
/ PRIOR APPLICATION NUMBER: 09/058,331  
/ PRIOR FILING DATE: 1998-04-09  
/ NUMBER OF SEQ ID NOS: 39  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 30  
/ LENGTH: 17  
/ TYPE: PRT  
/ ORGANISM: Sus scrofa  
US-09-281-760E-30

Query Match 47.8%; Score 65; DB 4; Length 17;  
Best Local Similarity 75.0%; Pred. No. 0.0013;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIVRSI 16  
Db 2 CRVTHPDLKPILRSI 17

RESULT 7  
US-09-100-414B-95  
Sequence 95, Application US/09100414B  
Patent No. 6025468  
GENERAL INFORMATION:  
APPLICANT: Wang, Chang Y1  
TITLE OF INVENTION: NOVEL LHRH PEPTIDE  
TITLE OF INVENTION: IMMUNOGENS  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan & Flinnegan, L.L.P.  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10154-0054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC Windows  
SOFTWARE: Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/100,414B  
FILING DATE: 20-JUNE-1998  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-100-414B-95

Query Match 47.1%; Score 64; DB 3; Length 25;  
Best Local Similarity 64.7%; Pred. No. 0.0028;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTTHPLPKDIVSIK 18  
DB 8 RVTTHPLPKALMSTK 24

RESULT 8  
US-09-303-323-95  
Sequence 95, Application US/09303323  
Patent No. 6228987  
GENERAL INFORMATION:  
APPLICANT: Wang, Chang Y1  
TITLE OF INVENTION: NOVEL LHRH PEPTIDE  
TITLE OF INVENTION: IMMUNOGENS  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan & Flinnegan, L.L.P.  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10154-0054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC Windows  
SOFTWARE: Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/303,323  
FILING DATE: 30-APR-1999

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/100,414  
FILING DATE: 20-JUNE-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-303-323-95

Query Match 47.1%; Score 64; DB 3; Length 25;  
Best Local Similarity 64.7%; Pred. No. 0.0028;  
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTTHPLPKDIVSIK 18  
DB 8 RVTTHPLPKALMSTK 24

RESULT 9  
US-09-770-014-95  
Sequence 95, Application US/09770014  
Patent No. 6559282  
GENERAL INFORMATION:  
APPLICANT: Wang, Chang Y1  
TITLE OF INVENTION: NOVEL LHRH PEPTIDE  
TITLE OF INVENTION: IMMUNOGENS  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan & Flinnegan, L.L.P.  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10154-0054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC Windows  
SOFTWARE: Word 97  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/770,014  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/100,414  
FILING DATE: 20-JUNE-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Maria H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4157  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-758-4800  
TELEFAX: 212-751-6849  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-770-014-95

Query Match 47.1%; Score 64; DB 4; Length 25;  
Best Local Similarity 64.7%; Pred. No. 0.0026;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18  
| | | | | : : : : :  
Db 8 RVTHPHLPALMRSTTK 24

## RESULT 10

US-09-701-588C-92  
; Sequence 92, Application US/09701588C  
; Patent No. 6713301

## GENERAL INFORMATION:

APPLICANT: UNITED BIOMEDICAL, INC., ET AL.  
TITLE OF INVENTION: ARTIFICIAL T HELPER CELL  
EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC  
PEPTIDE IMMUNOGENS

## NUMBER OF SEQUENCES: 151

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.  
STREET: 345 Park Avenue  
CITY: New York

STATE: NY  
COUNTRY: USA

ZIP: 10154-0054  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/701,588C

FILING DATE: 29-Nov. 6713301-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/100,414

FILING DATE: 20-JUNE-1998

ATTORNEY/AGENT INFORMATION:

NAME: Maria H. Iain

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4158PCI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 92:

US-09-701-588C-92

Query Match 47.1%; Score 64; DB 4; Length 25;

Best Local Similarity 64.7%; Pred. No. 0.0028;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18  
| | | | | : : : : :  
Db 8 RVTHPHLPALMRSTTK 24

## RESULT 11

US-09-701-623C-5

; Sequence 5, Application US/09701623C

; Patent No. 6811782

GENERAL INFORMATION:

APPLICANT: Wang Ph.D., Chang Yi

TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

ALLERGY

FILE REFERENCE: 11514153US1

CURRENT APPLICATION NUMBER: US/09/701,623C

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: PCT/US99/13959

; PRIOR FILING DATE: 1999-06-21

; PRIOR APPLICATION NUMBER: 09/100,287

; PRIOR FILING DATE: 1998-06-20

; NUMBER OF SEQ ID NOS: 91

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 25

; TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-701-623C-5

Query Match 47.1%; Score 64; DB 4; Length 25;

Best Local Similarity 64.7%; Pred. No. 0.0028;

Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18  
| | | | | : : : : :  
Db 8 RVTHPHLPALMRSTTK 24

## RESULT 12

US-09-701-623C-84

; Sequence 84, Application US/09701623C

; Patent No. 6811782

GENERAL INFORMATION:

APPLICANT: Wang Ph.D., Chang Yi

TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF

ALLERGY

FILE REFERENCE: 11514153US1

CURRENT APPLICATION NUMBER: US/09/701,623C

CURRENT FILING DATE: 2000-12-01

PRIOR APPLICATION NUMBER: PCT/US99/13959

PRIOR FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: 09/100,287

PRIOR FILING DATE: 1998-06-20

NUMBER OF SEQ ID NOS: 91

SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 84

; LENGTH: 25

; TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

US-09-701-623C-84

Query Match 46.3%; Score 63; DB 4; Length 25;

Best Local Similarity 68.8%; Pred. No. 0.004;

Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 VTHPHLPKDIVRSIAK 18  
| : | | | : : : : :  
Db 9 VSHPDLPREVRSIAK 24

## RESULT 13

US-09-281-760R-29

; Sequence 29, Application US/09281760R

; Patent No. 6734287

GENERAL INFORMATION:

APPLICANT: Lawton, Robert

APPLICANT: Metmer, Brian

APPLICANT: Francoeur, Greg

TITLE OF INVENTION: Specific Binding Protein for Treating

ALLERGY

FILE REFERENCE: 01-1275A

CURRENT APPLICATION NUMBER: US/09/281,760R

CURRENT FILING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: 09/058,331

PRIOR FILING DATE: 1998-04-09

NUMBER OF SEQ ID NOS: 39

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 29  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Felis catus  
US-09-281-7608-29

Query Match 44.1%; Score 61; DB 4; Length 17;  
Best Local Similarity 75.0%; Pred. No. 0.0053;  
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIYRSI 16  
Db 2 CRVTHPHLPDIYRSI 17

RESULT 14  
US-08-232-539D-19  
Sequence 19, Application US/08232539D  
Patent No. 5965709  
GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Ige Antagonists  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,539D  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/178583  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P3  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-232-539D-19

Query Match 44.1%; Score 60; DB 2; Length 22;  
Best Local Similarity 69.2%; Pred. No. 0.01;  
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIY 13  
Db 10 CRVTHPHLPALM 22

RESULT 15  
US-08-232-539D-20  
Sequence 20, Application US/08232539D  
Patent No. 5965709

GENERAL INFORMATION:  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Ige Antagonists  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,539D  
FILING DATE: 21-Apr-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/178583  
FILING DATE: 07-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744768  
FILING DATE: 14-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Svoboda, Craig G.  
REGISTRATION NUMBER: 39,044  
REFERENCE/DOCKET NUMBER: P0718P3  
TELEPHONE: 650/225-1489  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-232-539D-20

Query Match 44.1%; Score 60; DB 2; Length 24;  
Best Local Similarity 69.2%; Pred. No. 0.011;  
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPDIY 13  
Db 12 CRVTHPHLPALM 24

Search completed: February 22, 2005, 07:29:40  
Job time : 45 secs

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